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Branching Pattern Modeling for *Psychotoria* species and Their Deterministic Algorithm

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Method Article

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Abstract

Back Ground: The branching patterns and the subsequent elongations of two shrub *Psychotria* species, *Pyschotoria rubra* and *Psychotoria manillensis*, in Okinawa Island, the Ryukyu Islands, Japan, were examined by Watanabe. His results showed that Hamilton's classification for *Psychotria* species in the South American continent is also applicable to the same species in Okinawa Island. After Watanabe's research, the author of the present paper introduced branching pattern models for same species to simulate their branching patterns theoretically. He also determined the branching pattern models in earlier growth stages and calculated their occurrence probabilities. To proceed with the analyses, a systematic construction of the branching pattern models has been required.

Aims: To refine our earlier branching pattern models of *P. rubra* and *P. manillensis* in view of vector representation and to introduce a deterministic algorithm which produces the branching pattern models systematically.

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Methodology: Introducing vector representations, we refine previous branching pattern models for *Psychotria* species in Okinawa Island. We also study the properties of branching pattern models in view of computational methods. Finally, we describe a deterministic algorithm for branching pattern models of *P. rubra* and *P. manillensis* by a pseudo-code.

Results: By studying properties of branching patterns of *Psychotria* species in mathematical way, we systematize the construction of our branching pattern models as a deterministic algorithm. Running this algorithm, we also succeed in the determination of the third branching pattern models.

Conclusion: A systematic determination algorithm which produces the branching pattern models inductively has been successfully established.

Keywords: Pyschotoria rubra; Psychotoria manillensis; branching patterns; mathematical model; Okinawa Island.

2010 Mathematics Subject Classification: 92B99.

1 Introduction

For a long time, tree architecture has been attracting many scholars. Plant body aboveground consists of reputations of module structures which called shoots ([1]). Namely, tree architecture is formed by reputations of branching and subsequent elongations of branches ([2]). So it is important for the understanding of tree architecture to know the branching patterns and elongation patterns. In this paper, we focus our attention on branching pattern of certain subtropical tree species.

Hallé et al. [3] studied the structure of branching patterns of tropical trees and classified their branching patterns into twenty three patterns. Hamilton [4] showed that *Psychotria* species in the South American continent have three patterns in the classification. In the point of view of taxonomy, Sohmer and Davis [5] indicated the effectiveness of the Hamilton's results for *Psychotria* species in Philippines. Watanabe [6] studied the branching patterns and the subsequent elongations of *Psychotria rubra* and *Psychotria manillensis* in Okinawa Island. His results showed that Hamilton's classification of branching patterns for *Psychotria* species was also applicable to those in Okinawa Island. To simulate branching patterns of *P. rubra* and *P. manillensis* theoretically, in [7], the author of this paper introduced branching pattern models based on Watanabe's static datum. He also determined the branching pattern models in earlier growth stages and argued the properties of the branching patterns of *P. rubra* and *P. manillensis*. To proceed with our analyses, we need to construct further branching pattern models. However, there are some difficulties in the construction. Further branching pattern models are more complicated and the total number of these is so big. To overcome such difficulties, we introduce a deterministic algorithm for our branching pattern models in the present article. It is expected that the algorithm enable us to give a quantitative evaluation for the difference between branching patterns of *P. rubra* and *P. manillensis*. Indeed, we plan to calculate occurrence probabilities of further branching pattern models. Furthermore, by using these probabilities, we will also calculate Shannon-Wiener diversity indices for branching pattern models of *P. rubra* and *P. manillensis*. Finally, we will measure the difference between the branching patterns of two *Psychotria* species. It is an expected advantage of our algorithm.

This paper is organized as follows: In Section 2, we first recall fundamental features about branching patterns of *Psychotoria* species including Watabe's results. Taking these facts into consideration, we set ideal growth conditions. Furthermore, under these conditions, we introduce our branching pattern models for *P. rubra* and *P. manillensis*, which are called vector models. We also explain our intent of introducing vector models and compare them with other models. In particular, with a

famous theory for plant development, called L-system. In Section3, we constructed a deterministic algorithm which produce vector models inductively. By using the algorithm, we determine the first, second and third vector models in Section 4. Finally, we give the conclusions of this paper in Section 5. We also list all graphs associated with the third vector models in Appendix.

2 Branching Pattern Models for *Psychotoria* species

In this section, we first recall fundamental features of branching patterns of *Psychotoria* species. We also refine our branching pattern models for same species which were introduced in [7]

2.1 Fundamental Features of Branching Patterns

It is known that *Psychotoria* species flower at apices of their shoots. After flowering, new branches are produced directly under the apices. Hamilton [4] indicated that the three types Type 1 (Chamberlain), Type 2 (Leeuwenberg) and Type 3 (Koriba) occur as the branching patterns of *Psychotoria* species (see Fig. 1 below). In Type 1, a new branch appears directly under the apex and grows preserving the direction of the original branch. On the other hand, in Type 2, two new branches appear and both of them grow with new directions (i.e., they do not preserve the original direction of the old branch). In Type 3, we also have two new branches and one of them keeps the original direction and the other does not.

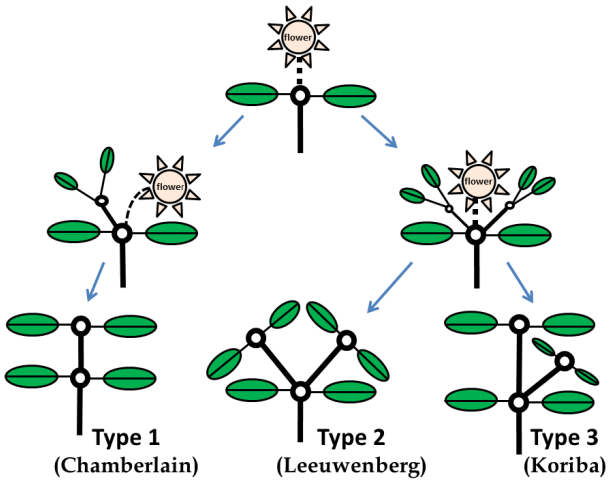

Fig. 1. Three fundamental branching patterns of *Psychotoria* species

In [6], Watanabe examined the branching patterns and the subsequent elongations of *P. rubra* and *P. manillensis* in Okinawa Island. They are two shrub *Psychotoria* speices spread in the Ryukyu Islands. Though they are allied species, they possess some different features. For example, their soil palatabillities are different. *P. rubra* prefers limestone area. By contrast with this, *P. manillensis* is widely distributed over non-limestone area. It is known that they are important component tree species in two different types of evergreen broad-leaved forests in the Ryukyu Islands, limestone forests and non-limestone forests respectively (see [8]). The research in [6] was conducted at two mountains in Okinawa Island, Mt. Nago-take (26352N, 128002E, 230m a.s.l.) for *P. rubra* and Katsuudake (26372N, 27562E, 320m a.s.l.) for *P. manillensis*. For both species, ten samples were randomly selected and their branching patterns were analyzed. Watanabe concluded

that Hamilton's classification of branching patterns of *Psychotoria* species is applicable to two *Psychotoria* species in Okinawa Island. He also found that the appearance rates of three branching patterns for two species were very different. *P. rubra* is formed by the reputations of the branching pattern Type 2. On the other hand, there is no bias in the branching patterns for *P. manillensis*.

2.2 Growth Conditions and Branching Pattern Models

In the construction of our mathematical models for *Psychotoria* species, we only pay attention to the branching patterns and ignore the other growth factors (e.g., elongations of branches, how to grow leaves etc.). Taking account of the fundamental features of branching patterns of *Psychotoria* species in Subsection 2.1, we always suppose that the growth of *Psychotoria* species satisfies the following ideal conditions:

Condition and Definition 2.1 (The growth conditions for *Psychotoria* species in Okinawa Island)**.** *The growth of Psychotoria species always satisfies the followings*:

1. *The germination always occurs. The sprout is described as one stem (see Fig. 2).*
2. *After the first flowering at the apex of the sprout, one of Type 1, Type 2 and Type 3 always occurs directly under the apex. We call plant bodies just after the first branching the first branching pattern models of Psychotoria species.*
3. *Inductively, for $l \geq 2$, we always have the lth branching after the lth flowering. It also occurs directly under the latest apices of an $(l-1)$th model. Here latest apices are defined to be the apices of shoots arose from the $(l-1)$th branching. We also call plant bodies just after the lth branching the lth branching pattern models of Psychotoria species.*
4. *Branches are never lost by abortion, withering and any other reasons.*

Remark 2.1. In [4], Hamilton showed that the transformations of Types 1, 2 and 3 were also occurred as the branching patterns of *Psychotoria* species in South American continent. However, Watanabe excluded these transformations in [6], because of the ambiguous of their definitions. We follow Watanabe's philosophy in this paper.

Remark 2.2. It is known that the frequency of flowering of *Psychotria* species depends on the regions where they live (see [9]). *P. rubra* and *P. manillensis* in Okinawa Island flower once a year. On the other hand, it was indicated that *Psychotria* species in Taiwan make flowers more than one time in a year.

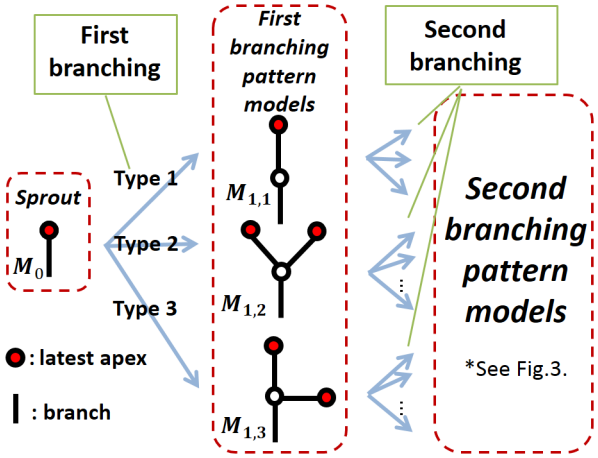

Fig. 2. The growth of *Psychotoria* species under the conditions 1-4

The growth of *Psychotoria* species in earlier stages is illustrated in Fig. 2. Note that the pictures in this figure only emphasize the number of shoots and whether new branches preserve the original directions or not. As mentioned above, the other factors of growth are all omitted. We call such pictures represent our branching pattern models *graphs*. All graphs associated with the first branching pattern models are easily determined as in Fig. 2. Taking account of all possible combinations of three fundamental branching patterns and latest apices of first branching pattern models, we can also obtain all graphs for the second branching models as in Fig. 3.

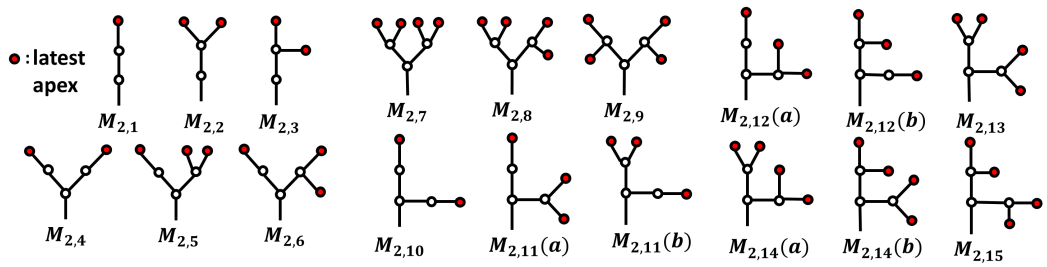

Fig. 3. All graphs associated with the second branching pattern models for *Psychotoria* species.

Fix a positive integer r. Let M be an rth branching pattern model for *Psychotoria* species. We denote by $m_r(M)$ the number of latest apices of M. If b_i is the number of Type i branching pattern occurrences in lth branching ($i = 1, 2, 3$ and $1 \leq l \leq r$), then we say the lth branching is given the vector $\boldsymbol{b} = (b_1, b_2, b_3)$.

Definition 2.1. We call a vector $\boldsymbol{b}$ which gives a branching pattern as above a branching vector.

Example 2.2. *For some branching pattern models in Figs. 2 and 3, we have*

$$m_1(M_{1,1}) = 1, \quad m_1(M_{1,2}) = 2, \quad m_1(M_{1,3}) = 2, \quad m_2(M_{2,1}) = 1, \quad m_2(M_{2,3}) = 2$$
$$m_2(M_{2,5}) = 3, \quad m_2(M_{2,6}) = 3, \quad m_2(M_{2,9}) = 4, \quad m_2(M_{2,10}) = 2, \quad m_2(M_{2,13}) = 4.$$

Example 2.3. *Type 1, Type 2 and Type 3 branching patterns in the first branching are expressed by the branching vectors* $\boldsymbol{b}_1 := (1, 0, 0)$, $\boldsymbol{b}_2 := (0, 1, 0)$ *and* $\boldsymbol{b}_3 := (0, 0, 1)$ *respectively.*

Example 2.4. *Since* $m_1(M_{1,1}) = 1$, *one of* $\boldsymbol{b}_1 = (1, 0, 0)$, $\boldsymbol{b}_2 = (0, 1, 0)$ *and* $\boldsymbol{b}_3 = (0, 0, 1)$ *can occur on the model* $M_{1,1}$ *as the second branching. On the other hand, only branching vectors* (i, j, k) *with* $i + j + k = 2$ *can be occurred on* $M_{1,2}$ *and* $M_{1,3}$ *as the second branching ,because* $m_1(M_{1,2}) = m_1(M_{1,3}) = 2$. *We determine all branching vectors that can occur as the second branching in Subsection 4.1.*

Note that an rth branching pattern model is yielded by successive r branching pattern occurrences. Let M be an rth branching pattern model which is yielded by $\boldsymbol{b}_{i_l}$ as its lth branching ($1 \leq l \leq r$). We identify M with the set of branching vectors $\{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_r}\}$. In particular, we formally express the sprout M_0 by the set $\{\emptyset\}$ which consists of an empty set. The growth of M is illustrated by the following sequence:

$$\{\emptyset\} \xrightarrow{\boldsymbol{b}_{i_1}} \{\boldsymbol{b}_{i_1}\} \xrightarrow{\boldsymbol{b}_{i_2}} \cdots \xrightarrow{\boldsymbol{b}_{i_l}} \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_l}\} \xrightarrow{\boldsymbol{b}_{i_{l+1}}} \cdots \xrightarrow{\boldsymbol{b}_{i_r}} M = \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_l}, \cdots, \boldsymbol{b}_{i_r}\}$$

Definition 2.2. Such branching pattern models as $M = \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_r}\}$ are called rth vector models.

From now on, we always consider the vector models.

Example 2.5. *We have the first vector models* $M_{1,1} = \{\boldsymbol{b}_1\}$, $M_{1,2} = \{\boldsymbol{b}_2\}$ *and* $M_{1,3} = \{\boldsymbol{b}_3\}$ *where* $\boldsymbol{b}_i$ $(i = 1, 2, 3)$ *are branching vectors defined in Example 2.3. Furthermore, a second branching* $\boldsymbol{b}_1$ *on* $M_{1,1}$ *yields a second vector model* $M_{2,1}$. *So we have the following sequence*:

$$\{\emptyset\} \xrightarrow{\boldsymbol{b}_1} M_{1,1} = \{\boldsymbol{b}_1\} \xrightarrow{\boldsymbol{b}_1} M_{2,1} = \{\boldsymbol{b}_1, \boldsymbol{b}_1\}$$

2.3 Vector Models Versus other Models

Plenty of methods has been proposed by many scholars to model the growth processes of plants (cf. [10] and references there in). In particular, geometrical models are plant architectural models described as algorithms of simulation which produce the forms and patterns of plants. They appeared in the 1960s with the development of modern computers (cf. Cohen [11], Honda [12] and Lindenmayer [13]). The topological structure of real plants consists of the genetically determined forms (described by the 23 patterns in [3]) and the deviations due to environmental factors. In the nature, environmental factors usually cause plants stochastic features in their growing process. These features make plants different from each other. Stochastic models are proposed to capture such phenomena. However, we only focus on genetic features of plants in this paper. Since vector models excluded environmental factors, they are more primitive than other growth models. For example, two branching pattern models (graphs) $M_{2,11}(a)$ and $M_{2,11}(b)$ in Fig. 3 are derived from same vector model, named $M_{2,11}$. Similarly, pairs of graphs $(M_{2,12}(a), M_{2,12}(b))$ and $(M_{2,14}(a), M_{2,14}(b))$ in Fig. 3 are given by vector models $M_{2,12}$ and $M_{2,14}$ respectively (the vector models $M_{2,11}$, $M_{2,12}$ and $M_{2,14}$ will be treated in Subsection 4.1). It is considered that further differentiation from one vector model is caused by environment factors. We believe the simpleness of vector models enable us to capture the essential features which only depend on plants themselves.

Here we compare vector models and a very popular mathematical theory for plant development, which is called Lindenmayer system (or L-system for short). It was introduced by Aristid Lindenmayer in [13]. This theory produces geometrical models which involve genetic and environmental informations. The essential difference between vector models and L-systems appears in the descriptions of generating branches. Our models produce new branches sequentially, whereas in L-systems branches are produced in parallel and simultaneously replaced.

3 A Deterministic Algorithm for Our Models

In this section, we explain our computational methods.

3.1 Auxiliary Lemmas

We fix notations and prove some lemmas needed later. We consider an rth vector model $M = \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_r}\}$ of *Psychotria* species. Let l be an integer with $1 \leq l \leq r$. By abuse of notations, we denote by $m_l(M)$ the number of latest apices of the lth vector model $\{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_l}\}$ associated with M.

Lemma 3.1. *Let* $M = \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_r}\}$ *be an* r*th vector model where* $\boldsymbol{b}_{i_l} = (b_{i_l 1}, b_{i_l 2}, b_{i_l 3})$ $(l = 1, \ldots, r)$. *For any integer* l *with* $1 \leq l \leq r$, *the following relation holds:*

$$m_l(M) = b_{i_l 1} + 2b_{i_l 2} + 2b_{i_l 3} \tag{3.1}$$

Similarly, for any integer l *with* $2 \leq l \leq r$, *we have*

$$m_{l-1}(M) = b_{i_l 1} + b_{i_l 2} + b_{i_l 3}. \tag{3.2}$$

Proof. We first prove the relation (3.1). If a Type 1 branching occurs in the lth branching, then one latest apex will be added to the lth vector model. On the hand, if one of the branching patterns Type 2 and Type 3 occurs in the lth branching, then the lth vector model obtains two new apices. The relation (3.1) follows from these facts. Next we consider the relation (3.2). Note that, for $\boldsymbol{b}_{i_l} = (b_{i_l 1}, b_{i_l 2}, b_{i_l 3})$, the total $b_{i_l 1} + b_{i_l 2} + b_{i_l 3}$ must coincide with the number of the latest apices of the $(l-1)$th vector model $\{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_{l-1}}\}$. Namely, the relation (3.2) holds. □

Proposition 3.1. *An rth vector model $M = \{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_r}\}$ exists if and only if the relation (3.2) holds for any l with $2 \leq l \leq r$.*

Proof. If a branching $\boldsymbol{b}_{i_l} = (b_{i_l 1}, b_{i_l 2}, b_{i_l 3})$ satisfies (3.2), then it can occur as the lth branching on the $(l-1)$th vector model $\{\boldsymbol{b}_{i_1}, \cdots, \boldsymbol{b}_{i_{l-1}}\}$. The "if part" has proven. The "only if part" is trivial. □

Define two sets A_l and B_l to be the set of all branching vectors which can occur as lth branching and that of all lth vector models respectively. We also set

$$C_l := \{m_l(M) | M \in B_l\}.$$

Definition 3.1. For a positive integer l with $1 \leq l \leq r$, we call the triple $\{A_l, B_l, C_l\}$ the data of the lth branching patterns. We also define $\{A_0, B_0, C_0\}$ to be the triple with $A_0 = \{\emptyset\}$, $B_0 = \{M_0 = \{\emptyset\}\}$ and $C_0 = \{1\}$.

3.2 Computational Methods

In this subsection, we introduce some computational methods. In particular, Algorithm 3.2 is our main result.

Proposition 3.2. *For l with $2 \leq l \leq r$, the set A_l is given by*

$$A_l = \{(b_1, b_2, b_3) | b_i \in \mathbb{Z}_{\geq 0}, b_1 + b_2 + b_3 \in C_{l-1}\}$$

where $\mathbb{Z}_{\geq 0}$ is the set of all non-negative integers.

Proof. Our assertion follows from the relation (3.2) in Lemma 3.1. □

Proposition 3.3. *For l with $2 \leq l \leq r$, the set B_l is constructed from A_l and B_{l-1} by the following algorithm*:

INPUT A_l *and* B_{l-1}
OUTPUT B_l
DEFINE $B_l = \emptyset$
FOR *each pair* $(\boldsymbol{b} = (b_1, b_2, b_3), M) \in A_l \times B_{l-1}$
IF $m_{l-1}(M) = b_1 + b_2 + b_3$ THEN *put* $B_l = B_l \cup \{M \cup \{\boldsymbol{b}\}\}$
ELSE *do nothing*

Proof. The necessary and sufficient condition for the occurrence of an lth branching pattern $\boldsymbol{b} = (b_1, b_2, b_3)$ on an $(l-1)$th vector model M is $m_{l-1}(M) = b_1 + b_2 + b_3$ by Proposition 3.1. In other words, an lth vector model $M \cup \{\boldsymbol{b}\}$ exists iff $m_{l-1}(M) = b_1 + b_2 + b_3$ holds. Furthermore, it is clear that this algorithm terminates in finite steps. □

The language described Proposition 3.3 is a pseudo-code. Pseudo-codes are not computer programs, but are more structured than usual prose. In particular, they are mixture of natural language and familiar structure from programming language. About pseudo-codes, refer to [14]. Pseudo-codes are not only used in information theory, but also in mathematics (cf. [[15], Appendix B]).

Proposition 3.4. *We have*

$$C_l = \{b_1 + 2b_2 + 2b_3 | \, (b_1, b_2, b_3) \in A_l\}.$$

Proof. Our assertion follows from the definition of C_l and (3.1) in Lemma 3.1. □

Algorithm 3.2 (Deteministic Algorithm for Vector Models)**.** *Let $\{A_0, B_0, C_0\}$ be the triple defined in Definition 3.1. For a given positive integer r, the data $\{A_r, B_r, C_r\}$ of the rth branching patterns is completely determined by the following finite steps*:

Step l - (i) $(l = 1, \ldots, r)$: *Determine A_l by Proposition 3.2 (i.e. collecting all triples (b_1, b_2, b_3) of non-negative integers which satisfy $b_1 + b_2 + b_3 \in C_{l-1}$).*

Step l - (ii): *Determine B_l from A_l and B_{l-1} by Proposition 3.3.*

Step l - (iii): *Determine C_l by Proposition 3.4.*

Proof. Our assertion follows from Proposition 3.2, 3.3 and 3.4. □

4 Application of the Algorithm

In this section, we determine all the first, second and third vector models by Algorithm 3.2. Though the first and second vector models already had obtained in [7], we revisit them in view of our new computational methods.

4.1 First, Second and Third Vector Models

For $r = 3$, we run Algorithm 3.2. We first do Step 1-(i) in Algorithm 3.2. By Proposition 3.2 with $C_0 = \{1\}$, we easily obtain $A_1 = \{\boldsymbol{b}_1, \boldsymbol{b}_2, \boldsymbol{b}_3\}$ where $\boldsymbol{b}_1 = (1, 0, 0)$, $\boldsymbol{b}_2 = (0, 1, 0)$ and $\boldsymbol{b}_3 = (0, 0, 1)$ (see Example 2.3). Next we add branching pattern $\boldsymbol{b}_i$ $(i = 1, 2, 3)$ to the sprout $M_0 = \{\emptyset\}$ as Step 1-(ii). Consequently, we obtain

$$M_{1,1} := M_0 \cup \{\boldsymbol{b}_1\} = \{\boldsymbol{b}_1\}, M_{1,2} := M_0 \cup \{\boldsymbol{b}_2\} = \{\boldsymbol{b}_2\}, M_{1,3} := M_0 \cup \{\boldsymbol{b}_3\} = \{\boldsymbol{b}_3\}.$$

Namely, we have $B_1 = \{M_{1,1}, M_{1,2}, M_{1,3}\}$. All first vector models are determined. As the final part of Step 1, we do Step 1-(iii). It follows from Proposition 3.4 and $\boldsymbol{b}_1 = (1, 0, 0)$, $\boldsymbol{b}_2 = (0, 1, 0)$ and $\boldsymbol{b}_3 = (0, 0, 1)$ that $C_1 = \{1, 2\}$. Step 1 has finished.

Similarly, we proceed with Step 2. As Step 2-(i), we determine the set A_2 of branching vectors which can appear in second branching. Same as Step 1-(i), the number $1 \in C_1$ yields the branching vectors $\boldsymbol{b}_1$, $\boldsymbol{b}_2$ and $\boldsymbol{b}_3$. On the other hand, for $2 \in C_1$, we consider all combinations of three non-negative integers b_1, b_2 and b_3 with $b_1 + b_2 + b_3 = 2$. It follows that the following 6 branching vectors:

$$\boldsymbol{b}_4 := (2, 0, 0), \boldsymbol{b}_5 := (1, 1, 0), \boldsymbol{b}_6 := (1, 0, 1), \boldsymbol{b}_7 := (0, 2, 0), \boldsymbol{b}_8 := (0, 1, 1), \boldsymbol{b}_9 := (0, 0, 2)$$

After all, we have $A_2 = \{\boldsymbol{b}_i | \, i = 1, \ldots, 9\}$. Next we apply Proposition 3.3 to A_2 and B_1 as Step 2-(ii). Note that the branching vectors $\boldsymbol{b}_1$, $\boldsymbol{b}_2$ and $\boldsymbol{b}_3$ are only elements in A_2 whose totals of all components are 1 and the vector model M_1 is an only element in B_1 whose number of latest apices is 1. So we combine each of $\boldsymbol{b}_1$, $\boldsymbol{b}_2$ and $\boldsymbol{b}_3$ and M_1. These combinations yield the following elements of B_2:

$$M_{2,1} := M_{1,1} \cup \{\boldsymbol{b}_1\} = \{\boldsymbol{b}_1, \boldsymbol{b}_1\}, M_{2,2} := M_{1,1} \cup \{\boldsymbol{b}_2\} = \{\boldsymbol{b}_1, \boldsymbol{b}_2\}, M_{2,3} := M_{1,1} \cup \{\boldsymbol{b}_3\} = \{\boldsymbol{b}_1, \boldsymbol{b}_3\}.$$

On the other hand, branching vectors $\boldsymbol{b}_i$ $(i = 4, \ldots, 9)$ have their totals of all components are 2 and two elements $M_{1,2}$ and $M_{1,3}$ in B_1 have two latest apices. Taking account of all combinations of these, we obtain the rests of elements in B_2 are determined as follows:

$$\begin{array}{llll} M_{2,4} := \{\boldsymbol{b}_2, \boldsymbol{b}_4\}, & M_{2,5} := \{\boldsymbol{b}_2, \boldsymbol{b}_5\}, & M_{2,6} := \{\boldsymbol{b}_2, \boldsymbol{b}_6\}, & M_{2,7} := \{\boldsymbol{b}_2, \boldsymbol{b}_7\} \\ M_{2,8} := \{\boldsymbol{b}_2, \boldsymbol{b}_8\}, & M_{2,9} := \{\boldsymbol{b}_2, \boldsymbol{b}_9\}, & M_{2,10} := \{\boldsymbol{b}_3, \boldsymbol{b}_4\}, & M_{2,11} := \{\boldsymbol{b}_3, \boldsymbol{b}_5\} \\ M_{2,12} := \{\boldsymbol{b}_3, \boldsymbol{b}_6\}, & M_{2,13} := \{\boldsymbol{b}_3, \boldsymbol{b}_7\}, & M_{2,14} := \{\boldsymbol{b}_3, \boldsymbol{b}_8\}, & M_{2,15} := \{\boldsymbol{b}_3, \boldsymbol{b}_9\} \end{array}$$

Hence, $B_2 = \{M_{2,i} | \, i = 1, \ldots, 15\}$. We do Step 2-(iii) as the final step of Step 2. It follows from Proposition 3.4 with $\boldsymbol{b}_i$ $(i = 1, \ldots, 9)$ that $C_2 = \{1, 2, 3, 4\}$. Step 2 has finished.

4.2 First, Second and Third Vector Models, Continued

Similar to subsection 4.1, the procedures for Step 3 can be performed. Step 3 yields the data of third branching patterns. Here we only list them below. We have

$$A_3 = A_2 \cup \{\boldsymbol{b}_i | \, i = 10, \ldots, 34\}$$

where

$$\begin{array}{llllll} \boldsymbol{b}_{10} := (3,0,0), & \boldsymbol{b}_{11} := (2,1,0), & \boldsymbol{b}_{12} := (2,0,1), & \boldsymbol{b}_{13} := (1,2,0), & \boldsymbol{b}_{14} := (1,1,1), & \boldsymbol{b}_{15} := (1,0,2) \\ \boldsymbol{b}_{16} := (0,3,0), & \boldsymbol{b}_{17} := (0,2,1), & \boldsymbol{b}_{18} := (0,1,2), & \boldsymbol{b}_{19} := (0,0,3), & \boldsymbol{b}_{20} := (4,0,0), & \boldsymbol{b}_{21} := (3,1,0) \\ \boldsymbol{b}_{22} := (3,0,1), & \boldsymbol{b}_{23} := (2,2,0), & \boldsymbol{b}_{24} := (2,1,1), & \boldsymbol{b}_{25} := (2,0,2), & \boldsymbol{b}_{26} := (1,3.0), & \boldsymbol{b}_{27} := (1,2,1) \\ \boldsymbol{b}_{28} := (1,1,2), & \boldsymbol{b}_{29} := (1,0,3), & \boldsymbol{b}_{30} := (0,4,0), & \boldsymbol{b}_{31} := (0,3,1), & \boldsymbol{b}_{32} := (0,2,2), & \boldsymbol{b}_{33} := (0,1,3) \\ \boldsymbol{b}_{34} := (0,0,4). & & & & & \end{array}$$

The set B_3 of all third vector models consists of the following 157 vector models:

$\{\boldsymbol{b}_1, \boldsymbol{b}_1, \boldsymbol{b}_i\}$ for $i = 1, 2, 3$
$\{\boldsymbol{b}_1, \boldsymbol{b}_i, \boldsymbol{b}_j\}$ for $i = 1, 2$ and $j = 4, \ldots, 9$
$\{\boldsymbol{b}_i, \boldsymbol{b}_4, \boldsymbol{b}_j\}$ for $i = 2, 3$ and $j = 4, \ldots, 9$
$\{\boldsymbol{b}_i, \boldsymbol{b}_j, \boldsymbol{b}_k\}$ for $i = 2, 3$, $j = 5, 6$ and $k = 10, \ldots, 19$
$\{\boldsymbol{b}_i, \boldsymbol{b}_j, \boldsymbol{b}_k\}$ for $i = 2, 3$, $j = 7, 8, 9$ and $k = 20, \ldots, 34$

We also have $C_3 = \{1, 2, 3, 4, 5, 6, 7, 8\}$. In Appendix below, we list all graphs associated with the third vector models.

5 Conclusions

The present paper provides the followings:

a In Section 2, we have introduced vector models for *P. rubra* and *P. manillensis*, which are the refinements of previous versions obtained in [7].

b In Section 3, we have constructed a deterministic algorithm to produce vector models for *P. rubra* and *P. manillensis* systematically.

c In Section 4, we determined all first, second and third vector models by using the algorithm.

Applying the deteministic algorithm, we have succeeded in the determinations of all first, second and third vector models. The application indicated that our algorithm is effective for the systematic construction of vector models for *P. rubra* and *P. manillensis*.

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Competing Interests

The author has declared that no competing interests exist.

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Appendix

In this appendix, we list all graphs arisen from the third vector models. As mentioned in subsection2.3, one vector model may give some graphs. In the determination of graphs, we identify two graphs which are considered to represent same plant in our real world (three dimensional space). Examples are given in Fig. 4.

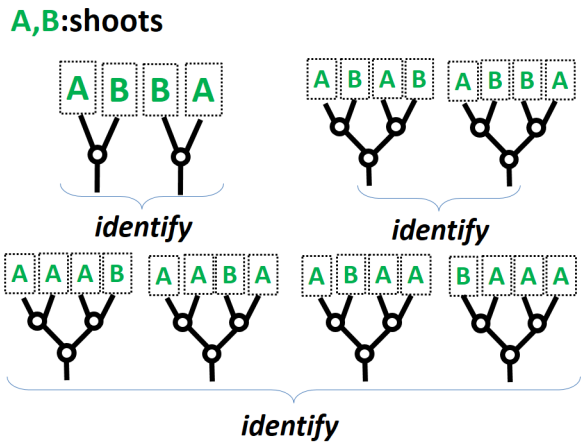
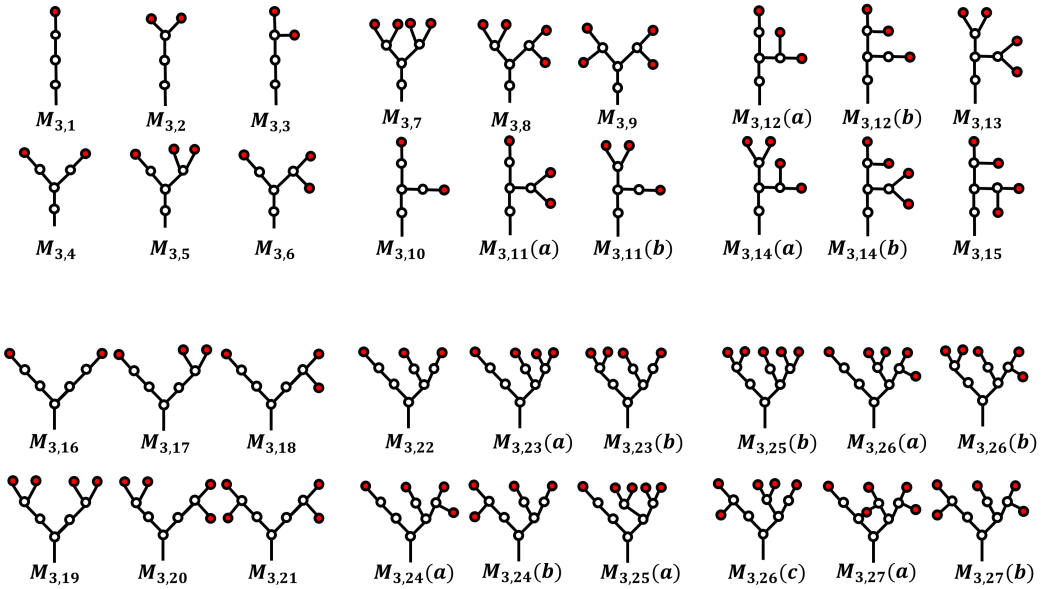
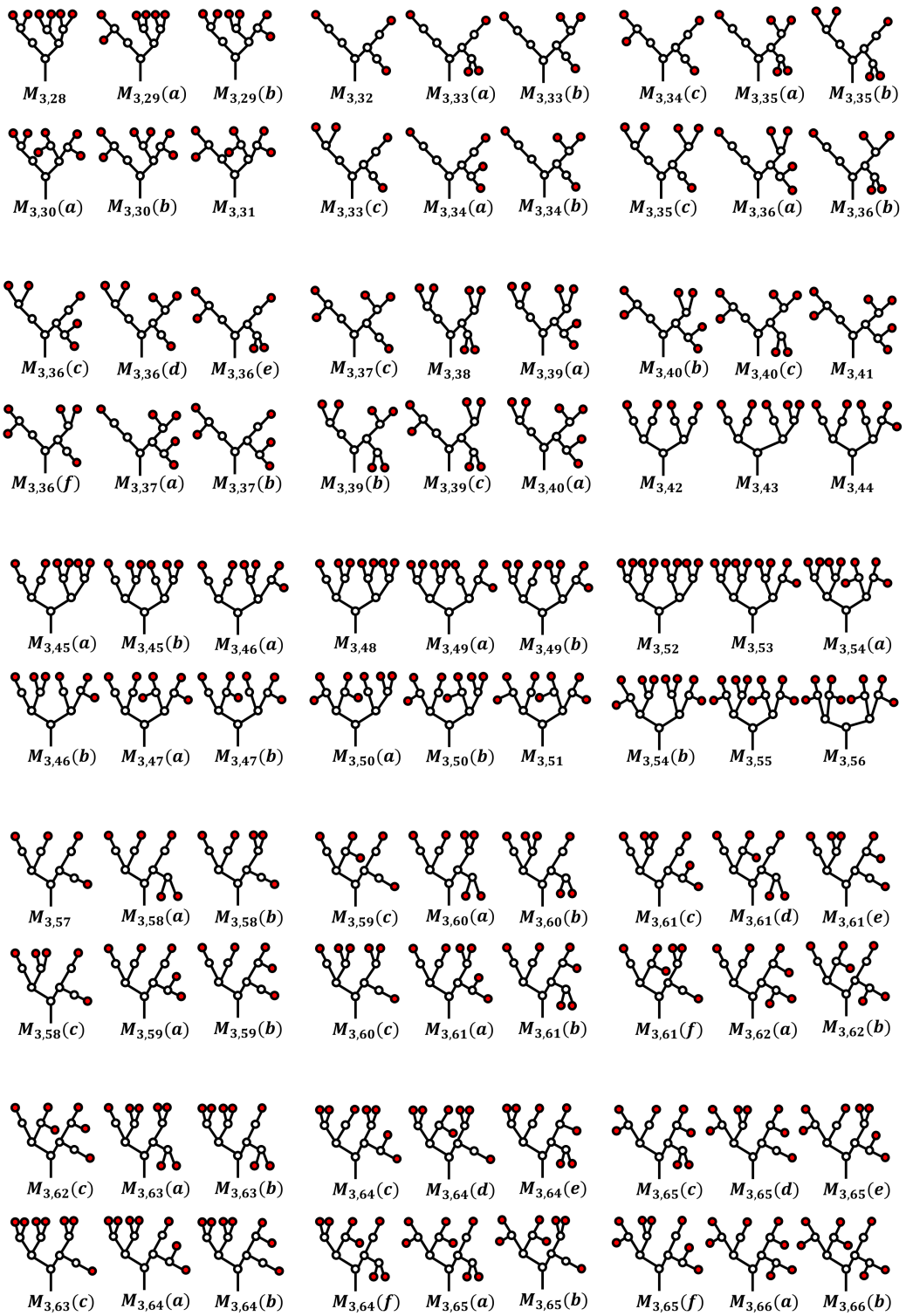


Fig. 4. Examples of identification of graphs

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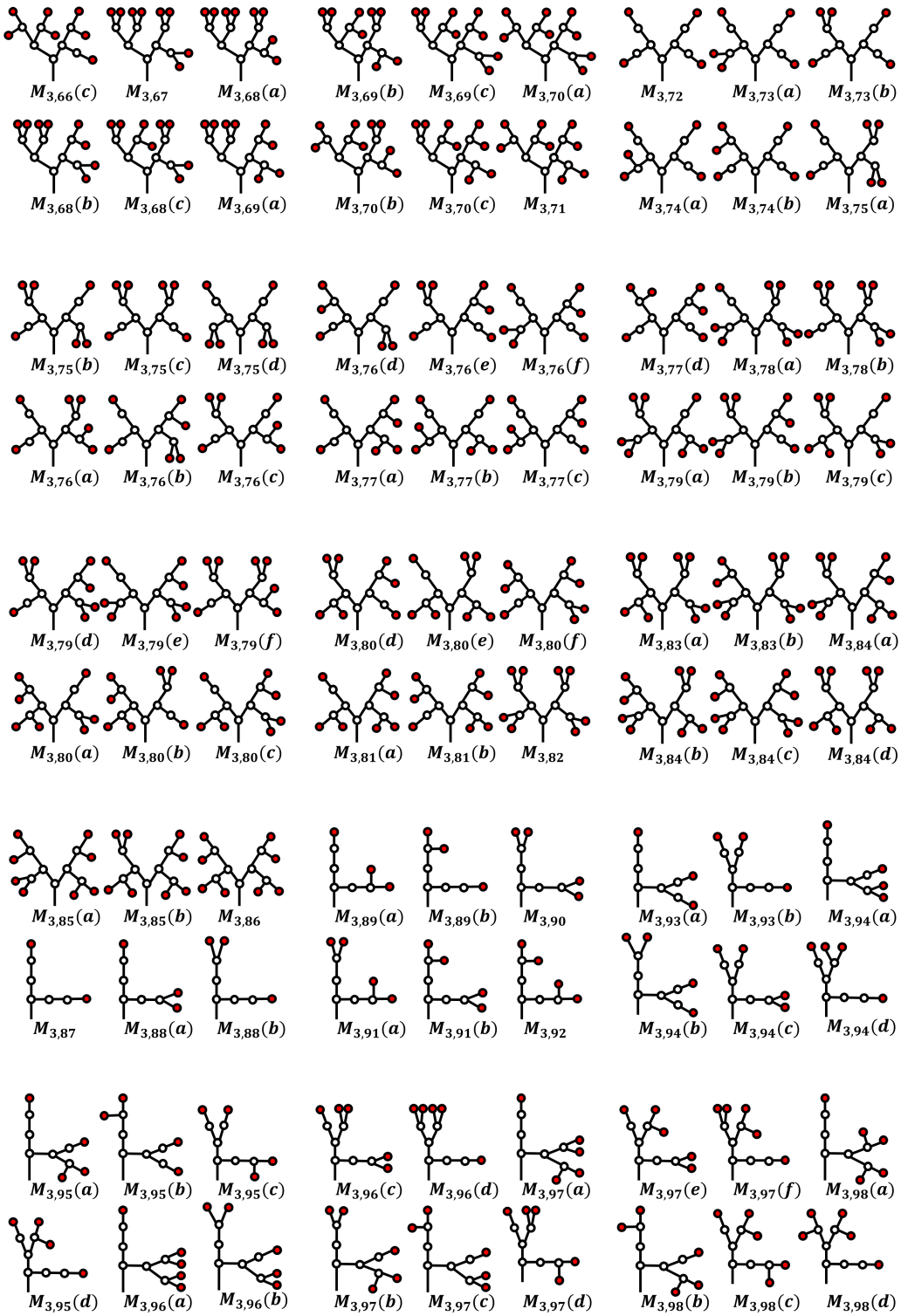
$M_{3,30}(a)$ $M_{3,30}(b)$ $M_{3,31}$ $M_{3,33}(c)$ $M_{3,34}(a)$ $M_{3,34}(b)$ $M_{3,35}(c)$ $M_{3,36}(a)$ $M_{3,36}(b)$
$M_{3,36}(c)$ $M_{3,36}(d)$ $M_{3,36}(e)$ $M_{3,37}(c)$ $M_{3,38}$ $M_{3,39}(a)$ $M_{3,40}(b)$ $M_{3,40}(c)$ $M_{3,41}$
$M_{3,36}(f)$ $M_{3,37}(a)$ $M_{3,37}(b)$ $M_{3,39}(b)$ $M_{3,39}(c)$ $M_{3,40}(a)$ $M_{3,42}$ $M_{3,43}$ $M_{3,44}$
$M_{3,45}(a)$ $M_{3,45}(b)$ $M_{3,46}(a)$ $M_{3,48}$ $M_{3,49}(a)$ $M_{3,49}(b)$ $M_{3,52}$ $M_{3,53}$ $M_{3,54}(a)$
$M_{3,46}(b)$ $M_{3,47}(a)$ $M_{3,47}(b)$ $M_{3,50}(a)$ $M_{3,50}(b)$ $M_{3,51}$ $M_{3,54}(b)$ $M_{3,55}$ $M_{3,56}$
$M_{3,57}$ $M_{3,58}(a)$ $M_{3,58}(b)$ $M_{3,59}(c)$ $M_{3,60}(a)$ $M_{3,60}(b)$ $M_{3,61}(c)$ $M_{3,61}(d)$ $M_{3,61}(e)$
$M_{3,58}(c)$ $M_{3,59}(a)$ $M_{3,59}(b)$ $M_{3,60}(c)$ $M_{3,61}(a)$ $M_{3,61}(b)$ $M_{3,61}(f)$ $M_{3,62}(a)$ $M_{3,62}(b)$
$M_{3,62}(c)$ $M_{3,63}(a)$ $M_{3,63}(b)$ $M_{3,64}(c)$ $M_{3,64}(d)$ $M_{3,64}(e)$ $M_{3,65}(c)$ $M_{3,65}(d)$ $M_{3,65}(e)$
$M_{3,63}(c)$ $M_{3,64}(a)$ $M_{3,64}(b)$ $M_{3,64}(f)$ $M_{3,65}(a)$ $M_{3,65}(b)$ $M_{3,65}(f)$ $M_{3,66}(a)$ $M_{3,66}(b)$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$M_{3,68}(b)$ $M_{3,68}(c)$ $M_{3,69}(a)$
$M_{3,70}(b)$ $M_{3,70}(c)$ $M_{3,71}$
$M_{3,74}(a)$ $M_{3,74}(b)$ $M_{3,75}(a)$
$M_{3,75}(b)$ $M_{3,75}(c)$ $M_{3,75}(d)$
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$M_{3,77}(d)$ $M_{3,78}(a)$ $M_{3,78}(b)$
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$M_{3,87}$ $M_{3,88}(a)$ $M_{3,88}(b)$
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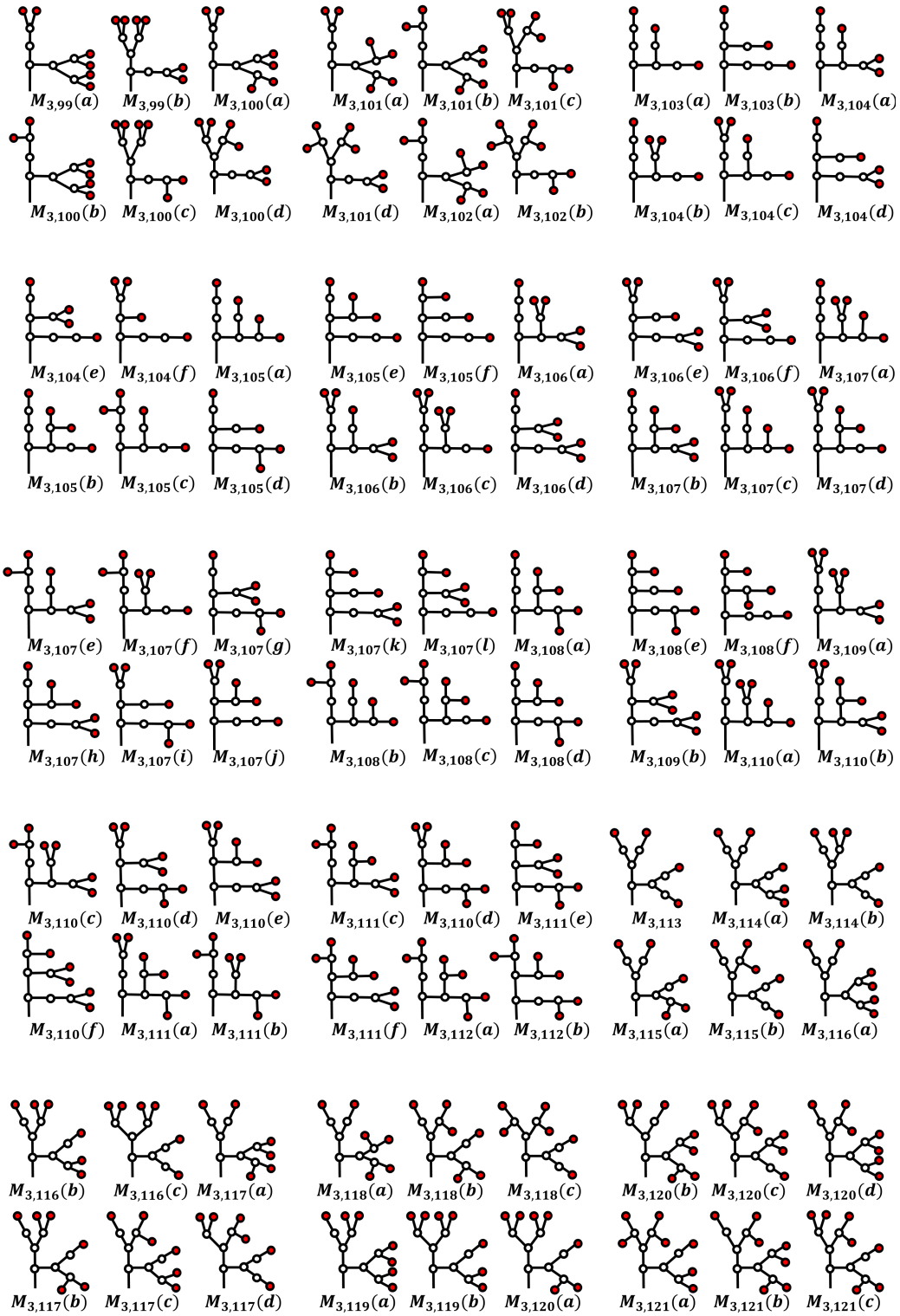
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$M_{3,100}(b)$ $M_{3,100}(c)$ $M_{3,100}(d)$ $M_{3,101}(d)$ $M_{3,102}(a)$ $M_{3,102}(b)$ $M_{3,104}(b)$ $M_{3,104}(c)$ $M_{3,104}(d)$
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$M_{3,107}(h)$ $M_{3,107}(i)$ $M_{3,107}(j)$ $M_{3,108}(b)$ $M_{3,108}(c)$ $M_{3,108}(d)$ $M_{3,109}(b)$ $M_{3,110}(a)$ $M_{3,110}(b)$
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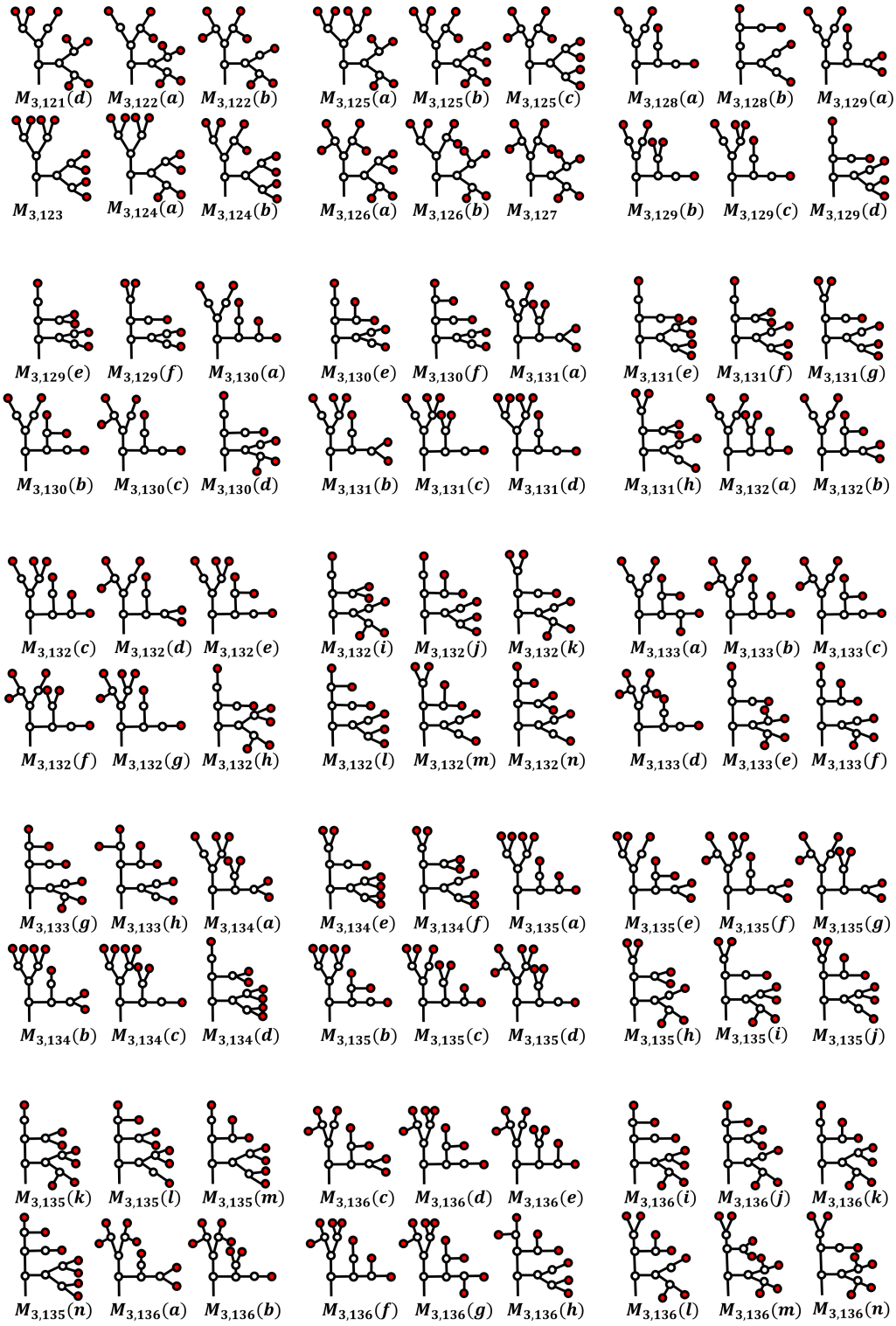
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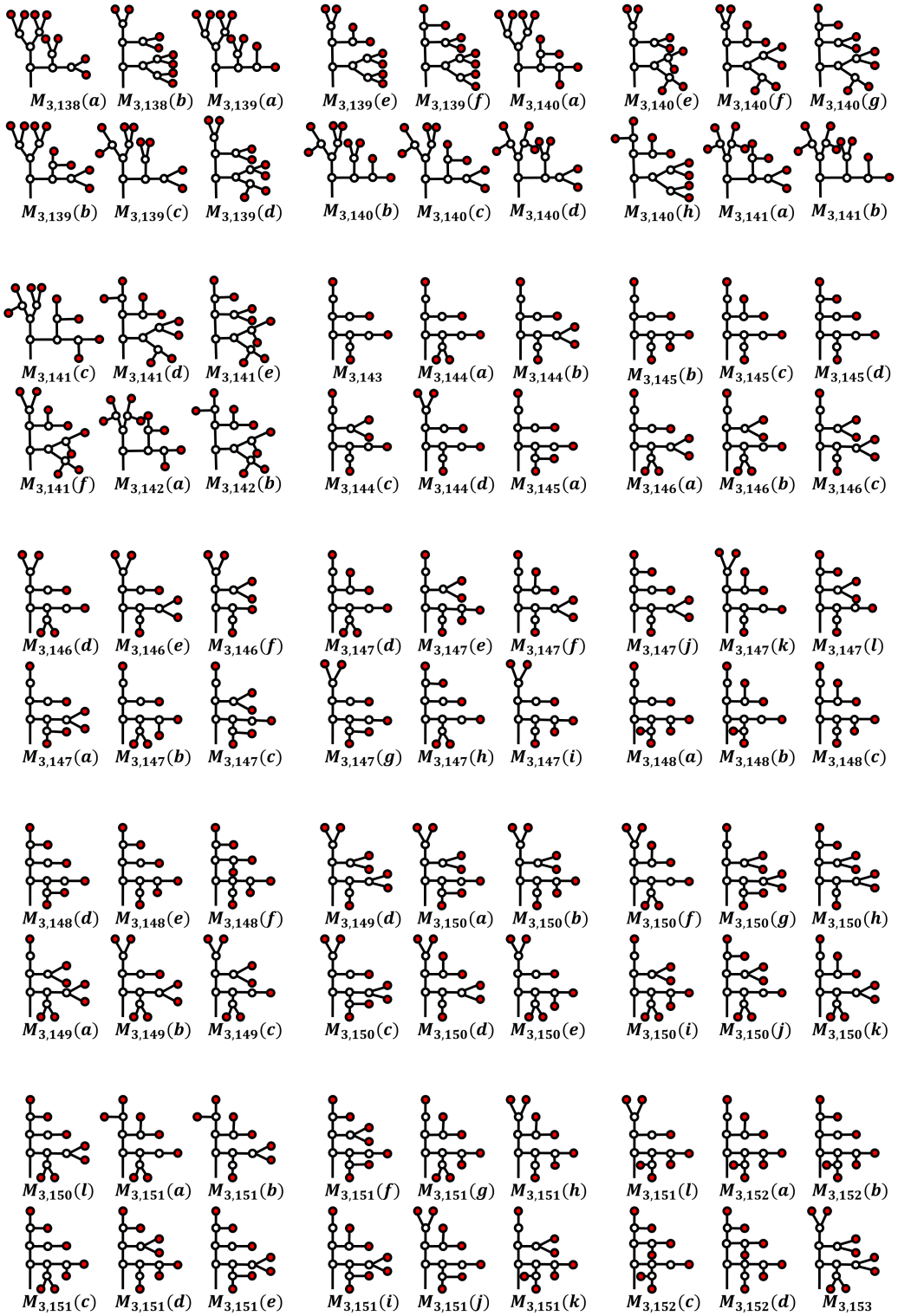
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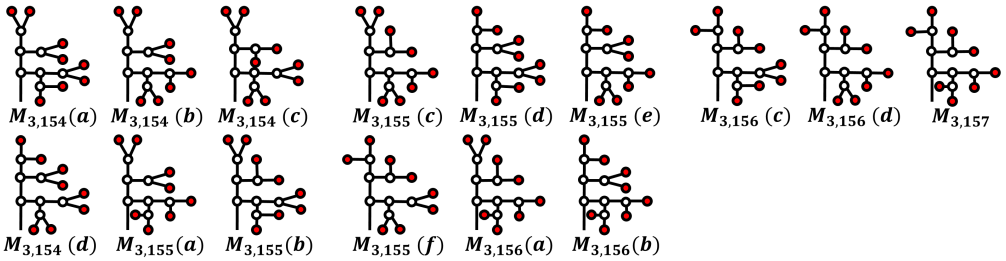

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