Karyotypic phylogeny and polyploidy variations of Paronychia (Caryophyllaceae) taxa in Turkey

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Abstract: Chromosomal data can provide very valuable information about karyotypic phylogeny and speciation. This is the first study on karyotype phylogeny and polyploidy variations of the genus Paronychia. In this context, the results are these: (1) in 14 taxa, the first report on chromosomes numbers; (2) in 2 taxa, equal chromosome numbers as in the previous report; (3) in all taxa, the first report of detailed karyotype analyses; (4) karyotype asymmetry data and generally symmetrical karyotypes; (5) karyotypic variations by mechanisms of dysploidy and polyploidy; and (6) phylogenetic relationships in Paronychia. The data indicate that Anatolia is an important area for the distribution of Paronychia. In light of all data, karyotype evolution is briefly summarized. The ancestral karyotype was $x = 9$ (millions of years ago). The karyotypes ($x = 8$ and $x = 7$) were then shaped by dysploidy. The rate of polyploidization then significantly increased in the genus. However, data should be supported by molecular analysis. In addition, the chromosome numbers of 8 species of Turkish Paronychia is still unknown. The determination of the karyological data of all species is very important to understand karyotype evolution and chromosomal phylogeny in Paronychia.

Key words: Karyology, Paronychia, phylogeny, polyploidy, Anatolia

1. Introduction
Karyotype evolution can be constructed with chromosomal features based on size, shape, and number. Karyotypic differences are one of the most important mechanisms supporting speciation as they may create transitional barriers between species (Baltisberger and Hörandl, 2016). Therefore, chromosomal characters are used to elucidate phylogenetic relationships in plant cytotomy. (Eroğlu et al., 2013; Eroğlu, 2015). These characters are basic number ($x$), diploid number ($2n$), chromosome length, relative length ($RL$), total haploid length ($THL$), centromeric index ($CI$), karyotype formula ($KF$), chromosome structure changes including deletions, inversions and translocations, chromosome number variations including dysploidy and polyploidy, karyotype asymmetry including symmetry/asymmetry index ($S/A$), the coefficient of variation of chromosome length ($C_{V_{chl}}$), and mean centromeric asymmetry ($M_{ca}$) (Peruzzi and Eroğlu, 2013; Eroğlu, 2015; Harpke et al., 2015; Baltisberger and Hörandl, 2016; Peruzzi et al., 2017; Şirin et al., 2019).

Karyotypic variations containing hybridization or polyploidization mechanisms are considered postcrossover barriers to speciation, diversification, and evolution of higher plants (Baltisberger and Hörandl, 2016). Almost all of the higher plants have undergone genomic duplication at least once in the history of evolution (Zhang et al., 2014). Glaciation, climate change, high altitudes, and high latitudes are important factors increasing polyploidy rates (Metzgar et al., 2016; Demirci Kayıran and Özhatay, 2017).

Paronychia Miller is a polyphyletic genus of the family Caryophyllaceae. The genus contains approximately 110 annual and perennial species spread out all over the world except in South Asia and South Africa (Chaudhri, 1968). Turkey, Peru, Bolivia, and America are distribution centers of the Paronychia species (Bittirich, 1993). In particular, Turkey is a major center, with 29 species, 5 subspecies, 7 varieties, and a total of 41 taxa, including 16 endemic (Chaudhri, 1967; Eroğlu et al., 2017). Paronychia is an important model in the determination of karyotype evolution and interspecific phylogenetic relationships due to its global distribution, different chromosome numbers, and especially because of its various ploidy levels. Anatolia, which includes 3 different phytogeographical areas such as the Mediterranean, Euro-Siberian, and Irano-Turanian regions.
regions, is an important place for the study of interspecific phylogenetic relations (Eroğlu et al., 2013).

Chromosome numbers are only given for 7 Turkish Paronychia. Four species are diploid; however, they exhibit 3 different basic numbers: \(x = 5 (2n = 10), x = 7 (2n = 14),\) and \(x = 9 (2n = 18).\) Six species are polyploid and reveal 2 different polyploidy levels of tetraploidy \((2n = 4x = 28 \text{ and } 36)\) and octoploidy \((2n = 8x = 56).\) P. argentea Lam. and P. polygonifolia (Vill.) DC. indicate high polyploidy \((8x).\) Three species are both diploid and polyploid (Lorenzo Andreu and García Sanz, 1950; Blackburn and Morton, 1957; Fedorov, 1974; Löve, 1975; Diosdado and Pastor, 1994; Runemark, 1996; Eroğlu et al., 2017). In Paronychia, the chromosomal reports are generally based on basic/diploid chromosome number without detailed chromosomal data. In the only existing report based on evolution and phylogeny, Alvarez (2010) examined 34 Paronychia species and 5 outgroups with chloroplast rps16 sequences and nuclear ITS sequences and reported that Paronychia is a polyphyletic genus divided into 2 different groups. In addition, North and South American species are sisters of the outgroup Gymnocarpos (Forssk.).

In Paronychia, the lack of chromosomal data and the absence of karyotypic phylogeny studies had an impact on the purpose and importance of this study. In this work, the aim is to contribute to the chromosomal data and karyotypic phylogeny of Paronychia taxa using the following marks: (1) chromosome number and karyotype formula, (2) detailed chromosome measurements, (3) karyotype symmetry/asymmetry, (4) polyploidy variations, and (5) karyotypic phylogeny.

2. Materials and methods
2.1. Plant material
Figure 1 shows a distribution map of Paronychia taxa. The collection information is listed below. All taxa except P. carica and P. chionaea subsp. chionaea are endemic to Turkey.

P. aksoyii Budak. Turkey. Erzurum: Tortum, near Tortumkale village, 1580-1620 m, 03-VII-2014, Budak 3060 & Hamzaoğlu (Bozok Hb.).

P. anatolica Czecz. subsp. balansae Chaudhri. Turkey. Izmir: Ödemiş, the east of Bozdağ sky center, 1610 m, 26-VI-2012, Budak 2642 & Hamzaoğlu (Bozok Hb.).

P. angrensis Chaudhri. Turkey. Ankara: over Beynam village, near Beynam forest entry, 1415 m, 13-VII-2013, Budak 2746 & Hamzaoğlu (Bozok Hb.).

P. argyroloba Stapf. Turkey. Antalya: between Korkuteli and Elmalı, near Ovacık village, 1475 m, 04-VII-2012, Budak 2650 & Hamzaoğlu (Bozok Hb.).

P. beauverdi Czecz. Turkey. Çankırı: between Eldivan and TRT transmitter, 1585 m, 11-VII-2013, Budak 2734 Hamzaoğlu (Bozok Hb.).

P. carica Chaudhri. Turkey. Denizli: Tavas, near Karahisar mine, 1420 m, 13-VII-2013, Budak 2741 & Hamzaoğlu (Bozok Hb.).

P. cataonica Chaudhri. Turkey. Malatya: Darende, near Çukurkaya village, 1340 m, 26-VI-2013, Budak 2718 & Hamzaoğlu (Bozok Hb.).

P. chionaea Boiss subsp. chionaea. Turkey. Bursa: below Soğukpınar, 950 m, 31-VII-2013, Budak 2752 & Hamzaoğlu (Bozok Hb.).

P. chionaea Boiss subsp. kemaliya Chaudhri. Turkey. Erzincan: Kemaliye, near Salihli village, 1450 m, 10-VII-2013, Budak 2732 & Hamzaoğlu (Bozok Hb.).

P. condensata Chaudhri. Turkey. Kayseri: Bakırdağ, near Yaylacık village, 1570 m, 15-VII-2012, Budak 2703 & Hamzaoğlu (Bozok Hb.).

P. davrazensis Budak. Turkey. Isparta: above Davrızsky center, 1920-1960 m, 10-VII-2014, Budak 3193 & Hamzaoğlu (Bozok Hb.).

P. galatica Chaudhri. Turkey. Kastamonu: near asphalt worksite of highway, 1037 m, 11-VII-2013, Budak 2736 & Hamzaoğlu (Bozok Hb.).

P. kurdica Boiss. subsp. hausknechtii Chaudhri. Turkey. Gaziantep: Sof mountain, hillsides, 965 m, 24-VI-2013, Budak 2711 & Hamzaoğlu (Bozok Hb.).

P. kurdica Boiss. subsp. montis-munzur Chaudhri. Turkey. Erzincan: between Erzincan and Pülümür, 1560 m, 12-VII-2012, Budak 2684 & Hamzaoğlu (Bozok Hb.).

P. saxatilis Chaudhri. Turkey. Van: Başkale, İspiriz Mountain, 3230-3260 m, 03-VII-2014, Budak 3010 & Hamzaoğlu (Bozok Hb.).

P. turcica Chaudhri. Turkey. Bitlis: between Tatvan and Gevaş, above Koruklu village, 1990 m, 02-VIII-2014, Budak 3298 & Hamzaoğlu (Bozok Hb.).

2.2. Cytogenetic procedure
The seeds were germinated between moist filter papers in petri dishes at room temperature. The root tips were then pretreated in α-monobromonaphthalene solution at 4 °C for 16 h, fixed in Carnoy’s fixative at 4 °C for 16 h, fixed in Carnoy’s fixative at 4 °C for 24 h, hydrolyzed in 1 N HCl at 60 °C for 12 min, and stained in 2% aceto-orcein for 2 h. Preparations were then made with the squash method (Altay et al., 2017; Martin et al., 2019).

2.3. Karyotype analysis
At least 10 well-spread metaphase plates were used to determine chromosome numbers. The chromosomal measurements were obtained by KaryoType software (Altnordu et al., 2016). The following parameters were used to characterize the chromosomes: short-arm length (SA), long-arm length (LA), total chromosome length = (SA + LA), total haploid length (THL), mean chromosome length (MHL), relative length (RL) = [(LA + SA)/THL] × 100, and centromeric index (CI) = [(SA)/(LA + SA)] × 100. Karyotype formulas were determined as described by Levan et al. (1964). The ideograms were drawn based on chromosome arm length.
2.4. Karyological relationships and karyotypic phylogeny

Karyological relationships were determined by following 8 parameters: [1] basic chromosome number (x), [2] diploid chromosome number (2n), [3] ploidy level (PL), [4] karyotype formula (KF), [5] total haploid length (THL), [6] mean centromeric asymmetry (M_{cl}), [7] coefficient of variation of chromosome length (CV_{cl}), and [8] symmetry/asymmetry index (S/A_{r}). The following 3 parameters calculated karyotype asymmetry, and these are M_{cl} (intrachromosomal asymmetry), CV_{cl} (interchromosomal asymmetry), and S/A_{r}. The formulae are given below.

M_{cl} = \frac{[\text{mean (L}_{L} - \text{S}_{L}) / (\text{L}_{L} + \text{S}_{L})] \times 100}{\text{L}_{L}}; \text{L}_{L}: total length of long arms and \text{S}_{L}: total length of short arms (Peruzzi and Eroğlu, 2013).

CV_{cl} = \frac{[\text{S}_{cl}/\text{X}_{cl}] \times 100}{\text{S}_{cl}}; \text{S}_{cl}: standard deviation and \text{X}_{cl}: mean chromosome length (Paszko, 2006). A scatter diagram was then drawn between the intrachromosomal asymmetry (M_{cl}) and interchromosomal asymmetry (CV_{cl}).

S/A_{r} = [(1 \times M) + (2 \times SM) + (3 \times ST) + (4 \times T)]/2n; M: median chromosome number, SM: submedian chromosome number: ST: subtelocentric chromosome number; and T: telocentric chromosome number. Unlike other methods, the S/A_{r} parameter is calculated using chromosome types and is classified into 5 karyotype types; these are [1] full symmetric (S/A_{r} = 1.0), [2] symmetric (1.0 < S/A_{r} ≤ 2.0), [3] between symmetric and asymmetric (2.0 < S/A_{r} ≤ 3.0), [4] asymmetric (3.0 < S/A_{r} < 4.0), and [5] full asymmetric (S/A_{r} = 4.0) (Eroğlu, 2015).

The phylogenetic tree showing karyological relationships was drawn by bootstrap values with UPGMA, chord coefficient. The phylogenetic tree contains the comparative phylogeny of the listed species. (1) 16 taxa from the present study, (2) 4 species from previous reports, namely P. adalia (Chaudhri), P. argentea, P. echinulata (Chater), and P. polygonifolia, with (3) Stellaria nemorum as the sister outgroup. The variables were then compared by Pearson correlations (PC) in Microsoft Excel software. The correlations were classified in the following order: [1] weak correlation (PC ≤ 0.25), [2] average correlation (0.25 < PC ≤ 0.50), [3] good correlation (0.50 < PC ≤ 0.75), and [4] high correlation (0.75 < PC) (P < 0.05).

3. Results

3.1. Chromosomal data

The chromosome records of 16 taxa are herein provided (Figure 2), 14 of which are reported for the first time. In addition, two of them (P. kurdica subsp. hausknecchi and P. kurdica subsp. montis-munzur) have similar numbers with previous data reported by Küpfer (1980). The chromosome numbers of Turkish Paronychia are given in Table 1, which also includes the results of present and previous studies. Six different chromosome numbers (2n = 18, 36, 52, 54, 72, and 104) are detected, 3 of which (2n = 52, 72, and 104) are new chromosome numbers for the genus. The smallest chromosome size among the taxa is 0.68 μm in P. kurdica subsp. hausknecchi. The largest chromosome size was detected in P. condensata, with 5.14 μm. The smallest total haploid length is 12.47 μm in P. kurdica subsp. hausknecchi, and the highest value is 87.48 μm in P. chionaea subsp. chionaea (Table 2).

3.2. Basic numbers, ploidy levels, and polyploidy

In genus Paronychia, there are generally 2 common basic numbers, which are x = 7 and most commonly x = 9. In this study, the basic chromosome numbers are x = 13 in P. chionaea subsp. kemaliya with ploidy levels of 4x/8x and x = 9 in the other taxa with ploidy levels of 2x, 4x, 4x/8x, and 6x (Table 1). The monoploid ideograms were generated by x = 9, and 13 are given in Figure 3.
Figure 2. Somatic metaphase chromosomes of A: *P. aksyvii*; B: *P. anatolica* subsp. *balansaes*; C: *P. angorensis*; D: *P. argyroloba*; E: *P. beauverdi*; F: *P. carica*; G: *P. cataonica*; H: tetraploid *P. chionacea* subsp. *chionacea*; I: octoploid *P. chionaea* subsp. *chionaea*; J: tetraploid *P. chionaea* subsp. *kemaliya*; K: octoploid *P. chionaea* subsp. *kemaliya*; L: *P. condensata*; M: *P. davrazensis*; N: *P. galatica*; O: *P. kurdica* subsp. *haustneckii*; P: *P. kurdica* subsp. *montis-munzur*; R: *P. saxatilis*; S: *P. turcica*.
Table 1. Chromosome numbers of Turkish Paronychia taxa (in alphabetical order).

| Paronychia                      | x  | 2n     |
|---------------------------------|----|--------|
| adelia                          | 9  | 36a    |
| amani                           | -  | Unknown|
| anatolica subsp. balansae       | 9  | 36     |
| angorensis                      | 9  | 36     |
| argentea                        | 7,9| 28b,36c,56d|
| argyroloba                      | 9  | 36     |
| aksoyii                         | 9  | 36     |
| beauverdii                      | 9  | 36     |
| boissieri                       | -  | Unknown|
| carica                          | 9  | 36     |
| catica                          | 9  | 54     |
| cephalotes                      | 9  | 36e    |
| chionaea subsp. chionaea        | 9  | 36,72  |
| chionaea subsp. kemaliya        | 13 | 52,104 |
| condensata                      | 9  | 36     |
| davorazensis                    | 9  | 36     |
| dudleyi                         | -  | Unknown|
| echinulata                      | 5,7| 10b,14d,28a|
| euphratica                      | -  | Unknown|
| galatica                        | 9  | 36     |
| kapela                          | 9  | 18,36e |
| kocii                           | -  | Unknown|
| kurdica subsp. hausknechtii     | 9  | 18b    |
| kurdica subsp. montis-munzur    | 9  | 18b    |
| macrosepala                     | 9  | 18b    |
| mughlaei                        | -  | Unknown|
| polygonifolia                   | 7  | 14,56b |
| pontica                         | -  | Unknown|
| saxatilis                       | 9  | 36     |
| sintenisii                      | -  | Unknown|
| turcica                         | 9  | 36     |

The chromosome arm lengths could not be measured in the octoploid *P. chionaea* subsp. *kemaliya* because the chromosomes are too small and the centromere is indeterminate.

3.3. Karyotype formulae and karyotype asymmetry

All taxa have median (m) and submedian (sm) chromosomes but not subtelo centric (s) and telo centric (t) chromosomes. Three different karyotype formulae are observed, which are M-m, m, and m-sm. In intrachromosomal asymmetry, the \( M_{CA} \) value ranges from 2.78 (P. kurdica subsp. *montis-munzur*) to 19.82 (P. argyroloba), which refers to symmetric karyotypes. In interchromosomal asymmetry, the \( CV_{CI} \) value ranges from 13.54 (P. cataonica) to 41.99 (P. kurdica subsp. *hausknechtii*), which refers to karyotype heterogeneity. In chromosomal type and centromeric position, the S/A, value ranges from 1.000 to 1.222, which refers to full symmetric and symmetric karyotypes, respectively (Table 2).

3.4. Phylogenetic analyses

Figure 4 shows a phylogenetic tree including the chromosomal data of present and previous studies in Turkish Paronychia. Sixteen taxa have variable ploidy levels (4x, 6x, and 4x/8x) and shape the clade I. The tetraploid taxa are quite dominant in subclade 1. In addition, subclade 2 contains high polyploid ratios and high chromosome numbers. In clade I, P. saxatilis, P. davorazensis, P. carica, P. argyroloba, and P. aksoyii are karyologically very close to each other. In the same way, P. turcica, P. angorensis, and P. anatolica subsp. *balansae* are also very close to each other karyologically.

Four taxa are diploid (2x) and shape the clade II. Subclade 3 contains the most symmetrical karyotypes in terms of intrachromosomal asymmetry. In contrast, P. echinulata has the most asymmetric karyotype and is located in subclade 4.

4. Discussion

4.1. Chromosome number

Table 1 demonstrates the chromosome numbers of the taxa investigated in the present study and in previous studies. The chromosome numbers are the first to be reported for 14 taxa. The chromosome numbers of P. kurdica subsp. *hausknechtii* and P. kurdica subsp. *montis-munzur* are the same as in the previous report, which is 2n = 18 (Küpf er, 1980). However, this taxon is *P. kurdica*, and it may be different from our subspecies.

Different chromosome numbers such as 2n = 18, 36, 52, 54, 72, and 104 are determined with a dominant number of 2n = 36. In the literature, there are different chromosome numbers such as 2n = 10, 14, 16, 18, 28, 32, 36, 42, 56, and 64 in genus *Paronychia* (for detailed references, see Table 1). Together with the present study, the chromosome numbers of the 8 taxa are still unknown in Turkey, namely *P. amani* Chaudhri, *P. boissieri* Rouy.
P. dudleyi Chaudhri, P. euphratica (Chaudhri) Chaudhri, P. kocii Budak, P. mughlaei Chaudhri, P. pontica (Borhidi) Chaudhri, and P. sintenisii Chaudhri. In this respect, the results of this study provide important contributions to the cytotaxonomy of Paronychia.

4.2. Basic number and karyotype formula

A basic chromosome number of $x = 9$ dominates in Turkish Paronychia taxa, but basic numbers of $x = 5, 7$, and 13 characterize several taxa. However, a basic chromosome number of $x = 8$ dominates in some regions such as Granada, Almeria in Spain, and Macaronesia, which is a phytogeographical region comprising the Azores, Madeira, the Canary Islands, and the Cape Verde Islands in the eastern North Atlantic. For example, the basic number is $x = 8$ in P. andina A. Gray, P. canariensis (L.) Link, P. depressa (Torr. & A. Gray) Nutt. ex A. Nelson, P. pulvinata A. Gray, P. sessiliflora Nutt., and P. suffruticosa (L.) Lam. (Hartman, 1972, 1974; Fedorov, 1974; Diosdado and Pastor, 1994; Suda et al., 2003).

All taxa have karyotypes containing M-m, m, and m-sm. In addition, the genus has the karyotypes with st chromosomes, which are 12m + 8sm + 2sm/st + 6st in P. argentea and m + 4sm + 6st in P. echinulata (Diosdado and Pastor, 1994).

4.3. Karyotype evolution; dysploidy and polyploidy

We believe that the ancestral basic number is probably $x = 9$ (Genome I), which is the dominant number. Then, the formations of the basic number such as $x = 8$ (Genome II) and $x = 7$ (Genome III) occurred with chromosomal changes such as fusion. Dysploidy is probably caused by fusion or reciprocal translocations of median chromosomes in ancestral karyotypes. Unlike the $x = 9$ karyotype, the karyotypes of $x = 7$ and 8 show lower diversity.

The polyploidy mechanism, which is quite common in genus Paronychia, appears to be the most important mechanism in the karyotype evolution of the genus. The first polyploidy mechanism probably occurred in ancestral karyotypes millions of years ago (Genome IV). Polyploid nature was demonstrated by the prevalence of cells with $2n = 4x = 36$ in many species, $2n = 4x = 52$ in P. chionaea subsp. kemaliya, $2n = 6x = 54$ in P. cataonica, $2n = 8x = 72$ in P. chionaea subsp. chionaea, and $2n = 8x = 104$ in...
We are of the opinion that Anatolia has a role in the distribution to other regions of *Paronychia* species for 2 reasons. The majority of taxa have a basic number of \( x = 9 \) and have a high polyploidy ratio. Polyploidy originates from autopolyploidy by genome duplication in a species and allopolyploidy by genome duplication between species and has played a major role in the speciation and evolution of higher plants (Demirci Kayıran and Özhatay, 2017). Polyploidy may affect the speciation of subspecies. Metzgar et al. (2016) reported that glaciation and associated climate shifts increased polyploidy rates. Demirci Kayıran and Özhatay (2017) reported that altitudes and high latitudes might have increased the polyploidy rates, although not always. All taxa have a distribution between 950 and 3260 m. High altitudes may have affected polyploidy levels, but this is not the only reason. For example, the adjacent cells of *P. chionaea* subsp. *kemaliya* have different patterns in terms of chromosome sets, which is the mixoploidy.

**4.4. Karyotype asymmetry**

In intrachromosomal asymmetry, all karyotypes are symmetrical except *P. echinulata*, *P. kurdica* subsp. *montis-munzur*, *P. kurdica* subsp. *hausknechtii*, and *P. beauverdii*, which have the most symmetrical karyotypes with 0

Figure 3. Ideograms of A: *P. aksoyii*; B: *P. anatolica* subsp. *balansae*; C: *P. angorensis*; D: *P. argyroloba*; E: *P. beauverdi*; F: *P. carica*; G: *P. chionaea* subsp. *chionaea*; H: *P. condensata*; I: *P. davrazensis*; J: *P. galatica*; K: *P. saxatilis*; L: *P. turcica*; M: *P. cataonica*; N: *P. kurdica* subsp. *hausknechtii*; O: *P. chionaea* subsp. *kemaliya*; P: *P. kurdica* subsp. *montis-munzur*.
< $M_{\text{CA}} \leq 10.00$, respectively. $P. kurdica$ subsp. montis-munzur and $P. kurdica$ subsp. hausknechti are diploid taxa (Table 2 and Figure 4). Table 3 presents a weak positive correlation between $M_{\text{CA}}$ values and ploidy levels ($r = 0.233$). In addition, the $M_{\text{CA}}$ value shows the correlations as weak or average in all parameters except with the karyotype formula and $S/A_I$ value, for which it correlates well. $P. argentea$ and $P. echinulata$ are rare species with subtelocentric chromosomes (Diosdado and Pastor, 1994), possibly due to the reciprocal translocations of the median/submedian chromosomes.

In interchromosomal asymmetry, all karyotypes are symmetrical except $P. kurdica$ subsp. hausknechti, $P. polygonifolia$, $P. echinulata$, $P. argentea$, and $P. cataonica$, which have the most symmetrical karyotypes with $0 < CV_{\text{CL}} \leq 15.00$, respectively. These taxa show diploidy in $P. polygonifolia$ and $P. echinulata$, polyploidy in $P. argentea$, and high polyploidy in $P. cataonica$ (Table 2 and Figure 4). Table 3 presents a negative average correlation between $CV_{\text{CL}}$ values and ploidy levels ($r = -0.452$). In addition, the $CV_{\text{CL}}$ value shows the correlations as weak or average in all parameters.

The most symmetric and asymmetric karyotypes are completely different between $M_{\text{CA}}$ and $CV_{\text{CL}}$ with a very weak correlation ($r = 0.014$) (Figure 5). All taxa have symmetrical karyotypes with only median/submedian chromosomes. As karyotype evolution progresses, chromosomal asymmetry continues to increase (Baltisberger and Hörandl, 2016). The fact that Anatolian $Paronychia$ taxa have symmetrical karyotypes with only median/submedian chromosomes may indicate that these taxa are in the early stages of karyotype evolution. These data support our opinion that Anatolia plays an important role in the distribution of the $Paronychia$ species. The asymmetric karyotypes are probably higher in other regions where the genus $Paronychia$ spreads.

4.5. Conclusion

In this study, the chromosomal data, polyploidy variations, and karyotypic phylogeny of 16 Turkish $Paronychia$ are shown. The data make up the first report for 14 taxa. The
The listed data provide important contributions to karyotype phylogeny and cytotaxonomy of *Paronychia*: (1) the majority of taxa have a basic number of $x = 9$, (2) high polyploidy rates, and (3) symmetrical karyotypes. The data support the fact that Anatolia is an important distribution center of *Paronychia*. However, it should be supported by molecular analysis. In addition, the chromosome numbers of 8 species from Turkey are still unknown. Determining the karyological data of all species is very important to understand karyotype evolution and chromosomal phylogeny of *Paronychia*.

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### Table 3. Pearson correlations for variables.

|       | $x$ | CN    | PL    | KF    | THL  | $M_{CA}$ | $CV_{CL}$ | S/A   |
|-------|-----|-------|-------|-------|------|----------|----------|-------|
| $x$   | 1   |       |       |       |      |          |          |       |
| CN    | 0.807 | 1     |       |       |      |          |          |       |
| PL    | 0.579 | 0.949* | 1     |       |      |          |          |       |
| KF    | -0.046 | -0.048 | -0.042 | 1    |      |          |          |       |
| THL   | 0.244 | 0.484 | 0.538 | 0.122 | 1    |          |          |       |
| $M_{CA}$ | 0.017 | 0.176 | 0.233 | 0.713 | 0.499 | 1        |          |       |
| $CV_{CL}$ | -0.098 | -0.365 | -0.452 | 0.124 | -0.410 | -0.013 | 1      |       |
| S/A   | -0.130 | -0.135 | -0.116 | 0.631 | 0.124 | 1.732    | 0.167    | 1     |

*Correlation is significant at the 0.05 level.

**Figure 5.** Scatter diagram between $M_{CA}$ and $CV_{CL}$.

- A: *P. aksayii*
- B: *P. beauverdi*
- C: *P. galatica*
- D: *P. anatolica* subsp. *balansae*
- E: *P. angorensis*
- F: *P. argyroloba*
- G: *P. carica*
- H: *P. cataonica*
- I: *P. chionaea* subsp. *chionaea*
- J: *P. chionaea* subsp. *kemaliya*
- K: *P. condensata*
- L: *P. davrazensis*
- M: *P. kurdica* subsp. *Hausknechtii*
- N: *P. kurdica* subsp. *montis-munzur*
- O: *P. saxatilis*
- P: *P. turcica*
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