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Contrastive analysis of trichome distribution, morphology, structure and associated gene expression reveals formation factors in different trichome types of two commercial Rosa species.

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Abstract: Trichomes are prevalent on the surfaces of many organs in Rosa and have an important impact on the edibility of the fruit. Here, the diversity, distribution, anatomical structure and genetic regulation of trichomes in Rosa roxburghii Tratt. (RR) and R. sterilis S. D. Shi (RS) are explored. RS and RR are important commercial crops in China due to their nutritional and medicinal values, however their consumption and utilization is limited, in part, by the abundance of trichomes on the fruit. There are two main forms of trichomes in both germplasms, namely glandular and non-glandular trichomes. Non-glandular flagellate and acicular trichomes are observed on the sepals, fruit, major leaf veins and pedicels of both germplasms, but non-glandular branched trichomes are present only on RS. Exfoliation of flagellate trichomes and lignification of acicular trichomes occur gradually on developing fruit. Capitate glandular and bowl-shaped glandular trichomes were abundant in RS, but were only observed on the major leaf veins of RR. Furthermore, some capitate glandular
trichomes on the pedicels were found to develop into prickles in RS. Transmission electron microscopy indicated that vacuolation and in the extraplasmic space occurred in the glandular cells of capitate trichomes at the late secretory stage. Prickles of RR and RS mainly consisted of lignin, suberin, cellulose and hemicellulose, however the ratios of these constituents varied between species. The expression levels of several well-known core trichome regulatory genes varied depending on the trichome types. The transcript abundance of GL1, GL2 and TTG1 was significantly higher in organs covered with acicular trichomes in both RR and RS, while the highest mRNA level of TRY was observed in glabrous organs, suggesting a negative effect of this gene on trichome formation. It was noteworthy that the negative regulatory factor CPC was only highly expressed in the leaf mesophyll of RR, where no glandular trichomes were present, but GL3, PDF2-like and CPC transcription factors co-regulated glandular trichome formation in RS. Expression of these genes peaked in the Fb3-stage buds of RR and B3-stage buds of RS, indicating different key phases for the regulation of trichome initiation. These data provide new insights into the genetic control of trichome formation in two Rosa species.

Keywords Rosa; trichome; morphology; prickle; gene expression

1. Introduction

Trichomes are present on the epidermal surfaces of leaves, stems, sarcocarps, fruits, seeds and other parts of many terrestrial plants (Chen et al., 2014). They originate from epidermal cells and are characterized by their morphology, including whether they are glandular or non-glandular, unicellular or multicellular, branched or non-branched (Werker, 2000). These structures can perform a range of functions for ecological interactions, such as protection against physical or biological stress (Karabourniotis et al., 2020). Furthermore, trichome structure has been used traditionally as an important factor in plant classification (Ma et al., 2016; Sajna et al., 2018).

The mechanisms of trichome initiation and development for unicellular trichomes have been extensively studied in Arabidopsis (Hülskamp, 2004; Schellmann and Hülskamp, 2005; Machado et al., 2009). Numerous
studies have identified a set of putative transcriptional regulators (comprising both positive and negative transcription factors) that control the process of epidermal cell development. The positive regulators include R2-R3 type MYB transcription factors GLABRA1 (GL1), the basic helix-loop-helix (bHLH) protein GLABRA3 (GL3) and the WD-repeat protein TRANSPARENT TESTA GLABRA1 (TTG1) (Walker et al., 1999; Zhang et al., 2003). These three positive regulatory proteins together activate trichome differentiation by enhancing the expression of GLABRA2 (GL2) (Serna, 2004). Single-repeat R3 MYB transcription factors CAPRICE (CPC), TRIPTYCHON (TRY), and transcriptional enhancers of TRY and CPC, such as ETC1 ETC2 and ETC3, competitively bind to bHLH factors when they move to the neighboring cells (Gan et al., 2011; Pesch and Hülskamp, 2011; Tominaga-Wada and Wada, 2017). However, unlike unicellular trichomes, relatively little is known about the development and regulatory networks of multicellular trichomes in plants.

*Rosa roxburghii* Tratt. (RR) is widely distributed in southwest and northwest China, whose fruits are valued for their high levels of ascorbic acid (AsA), superoxide dismutase activity and cancer-preventing effects. *R. sterilis* S. D. Shi (RS) similarly exhibits numerous nutritious and antioxidant activities. RR and RS fruits are being increasingly utilized as functional foods in the food industry to produce preserved foods and desserts, as well as in the beverage industry to produce wine, beer and soft drinks (He et al., 2016; Li et al., 2016). RR and RS belong to the Rosaceae family, and they have a very close genetic relationship based on RAPD and AFLP molecular markers (Wen and Deng, 2003; Wen et al., 2004). However, RR and RS differ in their appearance, the most significant of which are seed abortion and the differences in fruit shape, size and anatomy from RS to RR.

Trichomes are present on the buds, stems, pedicels and fruits of RR and RS, which affect the appearance and perceived quality of the fruits. However, to date, little is known about the formation or regulation of trichomes in these plants. Detailed analysis of trichome types and distribution in vegetative parts of *Rosa* have not been explored in previous studies (Caissard et al., 2006; Asano et al., 2008; Feng et al., 2015). However, He
et al., (1994) and Kellogg et al., (2010) explored the morphological diversity and anatomy in Rosa trichomes. We have also previously reported the types of trichome in two germplasms of Rosa roxburghii (Wang et al., 2019). However, the lack of structural studies and exploration of the molecular mechanisms on the development of trichomes have limited the elucidation of molecular pathways. As the current understanding of trichome distribution and development of RR and RS is insufficient, here we analyze the various forms of those structures on stems, sepal., fruit and pedicel in relation to the morphology, distribution, ultrastructure, and histochemistry of the trichomes. Furthermore, changes in relative expression levels of trichome-related genes (TRY, CPC, GL1, GL2, GL3, TTG1, PDF2 and PDF2-like), in both developing buds and in vitro organs with different types of trichomes, were studied to provide opportunities for improving the germplasm of Rosa through genetic engineering technologies.

2. Materials and methods

2.1 Plant material

10-year old trees of Rosa roxburghii Tratt. (RR) and R. sterilis S. D. Shi (RS) were obtained from the fruit germplasm repository of Guizhou University, Guiyang, China (26°42.408’N, 106°67.353’E). Samples were collected at random and immediately frozen in liquid nitrogen and stored at -80 °C until processed.

2.2 Stereo microscopy

The floral bud, stems, leaves, pedicels, sepals and fruits RR and RS were examined using a stereomicroscope (Zeiss Stemi 508) to characterize the types and distribution of trichomes. Samples of floral bud were collected from adult trees (n=30) in early March 2018. The stems, pedicels and sepals were collected from the middle and upper canopy of adult trees (n=30) in middle-late April 2018, and in middle-late August, ripening fruits were obtained from both RR and RS.

2.3 Light microscopy
To investigate the anatomical structure and development of trichomes, the stems, young fruit and floral buds of differing developmental stages of both RR and RS were fixed in formalin, alcohol and acetic acid solution (FAA)(mixture of 50% ethanol, 5% acetic acid, 3.7% formaldehyde, and 41.3% water). Samples were embedded in paraffin wax and longitudinal and transverse sections (6-8 μm thick) of stems and fruits were taken (Johansen, 1940). Sections were stained with 0.05 % toluidine blue (pH 4.3) and 0.5 % fast green, then examined and photographed using a Leica light microscope.

2.4 Scanning Electron Microscopy

The floral buds, young fruits, pedicels, bearing branches, sepals and stems were harvested at various stages of growth from RR and RS and were immediately fixed in 3 % glutaraldehyde solution in 0.1 M phosphate buffer at pH 7.2, overnight at 4 °C. The plant material was dehydrated through a tert-butanol and ethanol mixture series (30, 50, 70, 90, and finally 100 % concentration three times) then dried via vacuum cryodesiccation. Samples were next sputter-coated with gold and viewed using S-3400N scanning electron microscope to examine the type and morphology of trichomes (Ma et al., 2016). The prickles and various trichome types were measured in terms of their total length and basal width from > 20 images per organ.

2.5 Transmission Electron Microscopy

Samples of flagellate, acicular and capitate trichomes, and young prickles, from RR and RS were fixed in 3 % glutaraldehyde for 2 hours and washed thoroughly with 0.1 M phosphate buffer (pH 6.8). Afterwards, they are post-fixed with 1 % osmium tetroxide in phosphate buffer and subjected to following dehydration procedure in alcohol (50, 70, 80,90, and 100 %, each of 10 min), then two changes in 100 % acetone (each of 15 min), and embedded in epoxy resin. Ultrathin sections (80 nm) were transferred to formvar-coated grids and poststained with uranyl acetate and lead citrate (Ma et al., 2016). Observations were made with JEM-1200EX scanning transmission electron microscope at 120KV.
2.6 Flow cytometry analysis

Prickles from RR and RS were isolated and pooled as a sample and cells from the leaves of RR were used as a control. Nuclei from prickles or leaves were prepared and stained with 4’,6-diamidino2-phenylindole (DAPI) and a CyFlow Space (Sysmex, USA) analyzer was used to assess the relative DNA content in each sample (Galbraith et al., 2001).

2.7 Fourier transform infrared spectroscopy

Prickles from ripe fruits and stems of RR and RS were gently removed and pooled as a sample in mid August. The dry, milled lignin samples (sample and KBr tableting into a very thin film with a diameter of 13mm) were analyzed with a NICOLET iN10 MX Fourier transform infrared spectrometer, to investigate the IR bands and absorbance patterns of prickle and fruit spines, to assess the functional groups within the lignified cell wall (Li et al., 2012). Background spectra were taken in terms of every sample before getting sample spectra. Each spectrum was scanned 64 times across the range of 4000 to 600 cm\(^{-1}\), with a spectral resolution of 4 cm\(^{-1}\).

2.8 Total RNA extraction and qRT-PCR

Tissue samples were collected at varying stages of flower development: three samples were taken on a weekly basis from buds before shooting (B1-3), seven samples were taken through bud development during shooting every three days and finally samples were collected upon inflorescence (Fb1-7) (Fig. 1). Pericarp was sampled by gently pulling a razor over the young fruit and extracting a tissue sample of no more than 1 mm in thickness. Sarcocarp was sampled in an identical fashion, but here the tissue thickness can be up to 2 mm. Total RNA was extracted using a TRIzol RNA Purification Kit (TaKaRa, China). cDNA synthesis was performed according to the PrimeScript RT reagent Kit with gDNA Eraser protocol (TaKaRa, Kyoto, Japan). To identify genes of interest, sequences were compared between trichome related genes in *Arabidopsis* and a transcriptome.
database for RR and RS (unpublished), which was built by our group. Ubiquitin (UBQ) was used as reference gene to normalize the expression data. Primers used for qRT-PCR were designed with Primer Premier 6 software (Table 1). Quantitative RT-PCR (qRT-PCR) was performed on an ABI ViiA 7 DX system (Applied Biosystems) using SYBR Premix Ex Taq (TaKaRa). The relative gene expression level was calculated according to the $2^{-\Delta\Delta CT}$ method (Livak et al., 2001). Each experiment was performed in triplicate, and each time the experiment included three biological replicates.

3 Results

3.1 Morphology and structure of trichomes

Trichomes are abundant on the surfaces of both vegetative and reproductive organs of RR and RS, including the floral bud, stem, leaf, sepal, and fruit (Fig. 2). However, there are differences in the types of trichomes present on these organs. Broadly, the trichomes present on the surfaces of RR and RS could be split into two main categories: glandular trichomes and multicellular non-glandular trichomes. In RR, the glandular trichomes were only observed on the abaxial side of leaves (Fig. 2D). The prickles on the stem of RR are opposite and solitary on RS (Fig. 2C, 2I).

Scanning electron microscopy identified non-glandular trichomes including flagellate, acicular and branched forms, of varying size and distribution. Flagellate, multicellular and uniseriate trichomes with the distal end of the terminal cells delicate and greatly elongated (Fig. 3A, 3D, 3I). The flagellate trichomes were abundant on the surfaces of immature sepals and pedicels in RR and RS. The acicular trichomes, non-secretory multicellular trichomes were unbranched (Fig. 3A, 3B, 3E, 3H) and exhibited a higher variation in density and size in different organs. The acicular trichomes on immature sepals of RR have a wider base than those of RS (Fig. 3A, 3B).
Acicular trichomes were present on the immature pedicel of RR, but not in RS. However, the fruit bearing stem and immature stem surfaces of RR did not have trichomes. Unlike RR, RS had branched trichomes with six arms on its sepals (Fig. 3C). Two types glandular trichomes, capitate (Fig. 3B, 3F, 3G, 3J, 3O, 3P) and bowl-shaped glandular trichomes (Fig. 3Q), cover the epidermis of RS. The capitate glandular trichomes are multicellular, non-vascularized and composed of both epidermis and subjacent layers. They consist of glandular heads with multiple layers of epidermal cells and long stalks. The head of the glandular trichome has a wrinkled surface and the accumulation of a secretion was observed in the apical region of the head (Fig. 3G, 3K, 3P). Stomata were occasionally observed on the upper region of glandular heads (Fig. 3G, 3Q). The capitate glandular trichomes are distributed on the surface of many organs in RS but predominantly present on the sepals, immature pericarp and immature pedicel (Fig. 3B, 3F, 3J), and only small number were found on the immature stems (Fig. 3O). Bowl-shaped glandular trichomes were multicellular, non-vascularized, disc-shaped (patelliform) with a concave surface, and two mastoid structures in the center of the surface (Fig. 3Q). These were only observed on immature stems.

The types of trichomes observed and their distribution are provided in Table 2. Statistical analysis showed that the flagellate trichomes of RR and RS were statistically different in the size (P < 0.05). The acicular trichomes of RR are larger than RS on pericarp (P < 0.05), which were no difference in sepals. The capitate as trichomes of RR on the leaf abaxial were significantly larger than those found on all organs of RS (P < 0.05), well as of capitate trichomes head width (P < 0.05). The trichomes present on pedicels were characterized by having a larger size than trichomes found on all other organs of RS. It was noted that not only the length of prickles but also the basal width of prickles are larger in RR. Prickles reached a final height of 5.04 ± 0.36 mm and base width of 5.08 ± 0.26 mm in RR and final height of 3.18 ± 0.09 mm and base width of 3.939 ± 0.44 mm in RS (P < 0.05).
Acicular trichomes on the fruit of RR first developed in an erect manner, growing outwards, perpendicular to the fruit surface (Fig. 4A) and as they developed, they began to curve downwards, finally becoming sharp, pointed hooks with a broad base (Fig. 4B). Acicular trichomes on fruit of RS are widely spaced and small in size (Fig. 4D-E). Unlike acicular trichomes, capitate glandular trichomes grow both in length and in basal width, and fully mature to prickles (Fig. 4E, 4G). However, not all capitate glandular trichomes develop to prickles and there are still many capitate glandular trichomes on the mature fruit and pedicel (Fig. 4E, 4G). The capitate glandular trichomes of RS have faint yellow heads when young and wine-red when mature.

Longitudinally sliced tissue structure of matured prickles of RR and RS were studied using light microscopy (Fig. 5). Initial observations the prickles of RR and RS indicate that they are multicellular and non-vascularized. The surface of prickles was cornified and epidermal cells had thickened cell walls and enlarged vacuoles and were densely arranged. Prickles of RS consist predominantly of epidermal tissue (Fig. 5F), whereas prickles of RR are composed cells of both epidermal and cortical origin (Fig. 5C). Interestingly, a layer was observed which was comparable to the abscission layer of deciduous leaves in RS, however the prickles of RR did not exhibit this layer.

The ultrastructure of trichomes was explored using transmission electron microscopy (TEM). Acicular trichomes appeared highly vacuolated, with the cytoplasm restricted to a narrow peripheral band around the interior of the cell walls. The cells of acicular trichomes on the sepals of RR had different forms, but all were surrounded by a relatively thick cell wall (Fig. 6A, 6B). The epidermal cells were loosely arranged, and the intercellular spaces were large. The small amount of peripheral cytoplasm and plastids were aggregated in the corners of the cells, surrounding large vacuoles. The acicular trichomes on fruits of RR had a similar cellular morphology (Fig. 6C, 6D), the cell of acicular trichomes on fruits closely arranged and a few Golgi apparatus and mitochondria were found. In mature acicular trichomes of RS sepals (Fig. 6E, 6F), the most striking
ultrastructural features are the closely arranged cells, the high density of the cytoplasm, and the large size of the
nuclei, which also have prominent nucleoli. Plastids were present too, of varying size and shape, having electron
dense stroma and occasional starch grains. Vesicle-like structures of different sizes with an irregular outline
were also located in cytoplasm; some of these were translucent whilst others contained an osmiophilic core (Fig.
6G, 6H).

The flagellate trichomes of RR epidermal cells are long and closely arranged (Fig. 7A). They have thick
cell walls with a dense cytoplasm, vacuoles of varying size, large nuclei with prominent nucleoli, extensive
rough endoplasmic reticulum, and a zigzag-shaped structure. Various plastids had electron dense stroma and
occasional starch grains (Fig. 7B). Compared to the flagellate trichomes of RR, the epidermal cells of RS are
elliptic and plastids are ameboid or cup-shaped, many being electron-dense and occasionally containing starch
granules. Golgi stacks and rough endoplasmic reticulum occur infrequently (Fig. 7C, 7D).

The cells of young prickles in RR consist of densely arranged elliptic cells with a thick cell wall. Within
the cells, there are varying degrees of vacuolation and osmiophilic secretory material is localized adjacent to the
outer periclinal cell wall (Fig. 8A, 8B). Except the nucleolus, no other organelles were observed. The structure
of prickles in RS is broadly like those in RR (Fig. 8C, 8D).

Glandular trichomes on RS were selected to further study the structure of the capitate trichomes, whereby
ultra-thin sections sepal., fruit, pedicel, and stem were examined (Fig. 9). The capitate trichomes have common
and distinguishing features in all four organs. The glandular cells have large vacuoles which occupy the
majority of the cellular space, with cytoplasm located only in the peripheral region of the cells and numerous,
densely stained droplets of secretory product were observed in the periplasmic space. The glandular
cells contain starch granules and have plasmodesmata, although these are not as clearly visible in cells from the
sepal (Fig. 9A, 9B). The glandular cells from the sepal are markedly different, containing other organs and the
cells are polygonal in shape and loosely arranged.

The FTIR spectra of prickles from fruit are shown in Fig.10 (A, B). The spectra of RR and RS are largely similar, and the peaks predominantly ranged from 800-1800 cm\(^{-1}\). The main peaks, which are the stretching vibrations of -OH and suberin, are at 3403 and 2918 cm\(^{-1}\). The bands at 1452, 1383, 1250, 1157 and 1105 cm\(^{-1}\) are indicative of lignin and cellulose. However, between RR and RS, the relative intensity of peaks are different. The prickles on stems of RR and RS are mainly composed of lignin, suberin, cellulose and hemicellulose, but that the chemical composition of the prickle of stems is different (Fig. 10C, 10D). The FTIR absorbance was notably higher in the prickles from stems of RS than RR. Furthermore, the two species varied in the peak at 1379 cm\(^{-1}\); in RS this peak is intense but in RR it appears as little more than a shoulder.

To determine whether endoreduplication contributed to the enlarged RR and RS trichome cells, we measured the DNA content of mature fruit prickles using flow cytometry. As shown in Fig. 11, both RR and RS displayed a peak of DNA content at around 200. Surprisingly, no difference in nuclear ploidy levels was observed between fruit prickles and leaf tissue (2C), suggesting that RR and RS prickle cells did not undergo any endoreduplication.

### 3.2 Trichome-related gene expression in organs with different trichome types.

Above we report the distribution and structure of different types of trichomes, homogenous or heterogenous in their distribution over various organs, providing a basis for the exploration of regulatory mechanisms governing trichome formation and differentiation at specific developmental stages. Based upon previous findings about trichome formation factors in other plants, eight trichome-related genes were studied to assess their expression levels in organs with different types of trichomes according to quantitative PCR. Trichome-related genes expression displayed broadly consistent patterns in different trichomes types in some organs of RR and RS (Fig. 12). The expression levels of GL2, GL3, TTG1 and PDF2 is known to be
positively related to trichome formation, and here expression was higher in sepal II with acicular trichomes than
that in sepal I, which was covered with flagellate trichomes in RR, however, the expression levels of GL2 and
PDF2-like was significantly higher in sepal I. Furthermore, the gene which is negatively associated with
trichome formation, namely TRY, was significantly higher in sepal I, in which no acicular trichomes were
observed. Compared to sepal II, which had visible acicular trichomes and glandular trichomes in RS, the
expression of GL1, GL2, TTG1 and PDF2 was significantly higher in sepal I, and the surface of sepal I was
covered with flagellate and branched trichomes. CPC, a gene that has been known to function in suppressing
trichome initiation was significantly higher expressed in sepal I, compared to sepal II. Comparing the hairless
sarcocarp and pericarp, of which both were covered with acicular trichomes in RR, the expression levels of GL1,
GL2 and TTG1 were higher in the pericarp than the sarcocarp. The TRY gene also exhibits opposite trends with
the positive regulatory factors. The qPCR data presented here demonstrates that the expression levels of GL1,
GL2, GL3, TTG1 and PDF2-like were significantly higher in pericarp with acicular and glandular trichomes
than in sarcocarp of RS. In RR, the expression levels of GL1, GL2, and TTG1 were significantly higher in the
pedicel, with acicular and flagellate trichomes, than in the smooth bearing branch. In RS, the expression levels
of GL1, GL2, GL3, PDF2 and PDF2-like genes were significantly higher in the pedicel with flagellate and
glandular trichomes than in smooth bearing branch. Conversely, expression levels of CPC and TRY were
significantly higher in bearing branch than in the pedicel. The expression levels of GL1, GL2 and GL3 were
significantly higher in main veins, with profuse acicular and glandular trichomes, as compared to the mesophyll
layer, which has no trichomes. Moreover, CPC, the gene that has been known to play negative roles in trichome
formation, was highly expressed in mesophyll and lowly expressed in main veins. Overall, the expression level
of GL1, GL2 and TTG1 which are positively regulating trichomes formation are higher in covered with acicular
trichomes organs in RR, whereas the TRY inhibits trichome formation are expressed higher in lack of trichomes
Organs, and CPC only high expressed in mesophyll and higher expression level in in main vein or other trichomes organs, which might be associated with the glandular trichomes formation. Our results show that GL1 and Gl2 were expressed at higher levels in acicular trichome organs of RS. Moreover, GL3 and PDF2-like were very high expressed and CPC showed the lowest expression in densely glandular trichome organs which maybe shows that these genes significant linked the presence/absence and types of trichomes on the surface of RS.

3.3 Expression profiles of trichome-related genes during bud development

Expression of trichome-related genes in RR and RS were investigated during different stages of bud and floral bud development through qPCR (Fig. 13). Trichome-related genes correlated with bud growth and development. In RS, the total expression of GL1, GL2, GL3, PDF2-like, CPC and TRY follow a very similar trend through bud development, and the expression levels peaked in development stage B3. Although TTG1 and PDF2 have the same trend in bud development of RS, they do not peak at this stage. At the beginning of inflorescence, the positive regulatory genes and the negative regulatory genes showed an increasing trend and reached a peak on B3 in RS, while the trend of RR were slightly different. GL3, TTG1, PDF2, PDF2-like and TRY showed increased expression during bud development of RR, but did not reach a maximum value and begin to decrease again, except with PDF2. The relative expression levels of GL1 and CPC gradually decreased in RR during inflorescence. During inflorescence, the mRNA levels of positive regulatory genes GL3, TTG1, PDF2, PDF2-like and the negative regulatory gene CPC initially increased before decreasing in RS. However, the time required to reach peak was different; TTG1, PDF2-like and CPC were Fb3 and the rest were Fb4. In RR, trichome-related genes exhibited a similar pattern, in which initially expression increased then a subsequent decrease were observed, and the peak of almost all genes occurred in stage Fb3.

4 Discussion

Trichomes are hair-like structures that commonly present on the surface of branches, roots, leaves and
sepals (Chen et al., 2014; Haratym et al., 2015), and indeed some fruits are also thickly covered with trichomes. The surface of fruits of RR and RS are one such example, being densely covered with trichomes as seen in many species of the *Rosa* family. These trichomes have implications for fruit quality, cultivation, and processing (Singh et al., 2020). Here, two morphologically distinct trichome types were observed, namely glandular and non-glandular trichomes, which have been previously reported in the genus *Rosa*. (Wang et al., 2019). The external and internal features of trichome morphology and subcellular features of two main type trichomes and capitate glandular morphotype were analyzed together here for the first time in RR and RS.

Non-glandular trichomes of RR and RS were mainly flagellate and acicular trichomes. These are typical types of non-glandular trichomes from other *Rosa* species, including *Rosa* roxburghii Tratt f. esetosa Ku (Wang et al., 2019) and *Rosa hybrida* L. 'Radtko' (Kellogg et al., 2011). Acicular trichomes had a homogeneous distribution across sepals and fruit of RR and RS, being especially prevalent on the surface of RR fruit. Acicular trichomes are longer than other trichomes; their sharp tips can serve as a mechanical barrier and a defense mechanism for the plant (Fahn, 1952). It has been shown in *Withania somnifera* (L.) Dunal (Solanaceae) by Munien et al., (2015) that trichome density is closely related to insect pest resistance. Acicular trichomes of RR contained a multicellular basal pedestal, which serves to support the trichome and to provide a point of attachment that “anchors” the trichome to the epidermal surface (Fig. 3A, 4B, 5A). Our results found a difference in the structure of acicular trichomes in RR and RS (Fig.4B, 4E). Acicular trichomes of RS do not have as large a basal pedestal as RR which may be the reason for shedding easily from the surface of fruit with the maturing (Gallenmüller et al., 2015).

Flagellate trichomes are mainly distributed on the surfaces of sepals and pedicels in both species and flagellate trichomes of RS are longer than RR. Flagellate trichomes were more abundant in RR and were only present on immature organs (Fig. 3A, 3I). This phenomenon may be due to the mature organ’s establishment of
phytochemical defense mechanism, by which point they no longer need the protection of flagellate trichomes (Munien et al., 2015). Plastids were observed in the cells of flagellate trichomes, which likely contributed to the silver-white coloration on the sepal’s surface of RR and RS (Fig. 7A, 7D).

Compared with RR, RS had more abundant non-glandular trichome types. In addition to acicular and flagellate trichomes, there are branching trichomes which have not been observed in other Rosa species. Non-glandular trichomes have been shown to function in defense against insect herbivores including influencing oviposition, protection against UV light and low temperature, and facilitating seed dispersal (Karabourniotis, et al., 2020).

Our results showed that the greatest differences between trichomes of RR and RS were found in glandular trichomes. The glandular trichomes of RS were located on the surface of all above ground organs, however, in RR limited numbers of glandular trichomes could only be found on the abaxial side of leaves. This may indicate that some genes regulating glandular trichomes on RS have different regulatory pathways with RR, which is in agreement with the hypothesis suggested by Wen et al., (2004), whereby RS was suggested to originate from a mutant of male-sterile R. kweichonensis. RS carries both capitate and bowl-shaped glandular trichomes, but capitate glandular trichomes were most common. Capitate glandular trichomes were predominantly present on the pedicel and fruits, with sparse distribution on the bearing branch. Capitate glandular trichomes were multicellular, non-vascularized, thick stalked and had large head cells which were composed of 16-34 thin-walled cells, with a small number of pores visible in the center of the head (Fig. 3G, 3J, 3K). Stomata are frequently observed in the early developmental stages of glandular trichomes, corroborating previous work in Vitis davidii which showed that stomata on glandular trichomes form in the period of rapid cell proliferation and elongation of the upper region epidermal cells (Ma et al., 2016). The development of stomata was not observed in RS, however this may be a result of variance in the sampling period. The head of capitate trichomes often
secrete sticky mucilage to trap insects which can avoid the invasion of insects (Nogueira et al., 2013; Uzelac et al., 2017). Similarly, capitate glandular trichomes can secrete substances via pore-like openings on each of the multicellular head cells based on our observation (Fig. 3G). The nucleus is surrounded by plastids containing starch grains and plastoglobuli, and the cytoplasm contains osmiophilic droplets, mitochondria and endoplasmic reticulum, all of which, in combination, are considered to be evidence of secretory activity in a range of angiosperm taxa (Haratym et al., 2017). However, we observed the ultrastructure of the head of capitate trichome in RS and did not see evidence for such secretion. It may be the case that these trichomes are only secretory at specific developmental stages.

During observation of the pedicel of RS (Fig. 3J, 4F, 5E), we initially only saw capitate glandular and flagellate trichomes from tissues harvested in April. As time progressed, prickles were observed on the surfaces of RS pedicels, however our sampling schedule did not allow us to see the early developmental stages of these prickles. Morphologically, there is no difference between glandular trichomes and prickles, but prickles are more robust (Coyner et al., 2005). We surmise that the prickles undergo early developmental stages like other capitate glandular trichomes (Fig. 3J) and once some capitate glandular trichomes have reached the post-secretory phase (Fig. 3G), the heads are shed and they increase in both height and basal width, thus developing into prickles (Fig. 4G). Therefore, it is reasonable to presume that the prickles of RS are homologous to capitate glandular trichomes. Rose and raspberry prickles progress through the four stages: (I) prickle is defined simply as a mass of proliferating cells, (II) a stalk emerges from the epidermis at the base of the cell mass and lifting it distally from the stem, (III) the distal cell mass falls off the stalk, followed by cell expansion in the stalk, (IV) the prickle is lignified and growth halted (Kellogg et al., 2011). This progress is similar with RS. However, it is important to note that only a small subset of glandular trichomes complete this final stage of development and form prickles in RS (Fig. 1F, G, 4E, 4G), this differs from Vitis. Davidii, where all form
prickles (Ma et al., 2016). The glandular trichome head may send signals to the epidermal and/or cortical organs that cause a proliferation of cells, allowing a prickle to develop (Kellogg, 2011).

Prickles lack internal vascular material and result from multiple cellular divisions of the epidermis (Fig. 5C, 5F). The dense cytoplasm had begun to degenerate, with reduced numbers of organelles visible and was located only in the peripheral region of the cells (Fig. 8). A layer was observed which resembled an abscission zone at the base of prickles of RS, where they meet the epidermis (Fig. 5F). Both mature and young prickles could be broken off with little force at this layer, suggesting this abscission zone fully forms early on in the prickle’s development. The prickles of RR do not have such a zone (Fig. 5C), but it was previously reported in the prickles of Rosa hybrida cv. “Laura” and “Queen Elizabeth” (Asano et al., 2008, Li et al., 2012).

Analysis by FTIR showed that prickles on the fruit surface and stem of RR and RS consisted mainly of cellulose, hemicellulose, cork and lignin, but there were significant differences in the relative abundance of these compounds. These findings were similar to previous studies on wood (Asano et al., 2008; Le et al., 2017). Li et al., 2012 studied the anatomical structure and chemical composition in prickles of Rosa hybrida, and found that differences in chemical composition of prickles maybe related to the strength with which the prickle adheres to the stem. The concentration of cellulose, hemicellulose, cork and lignin in prickles were higher in RS than RR, both on the fruit surface and stem. This difference may be one of the reasons why prickles on RS are more weakly adhered than those on RR when the fruit is ripe.

Genetic analysis in Arabidopsis has established a regulatory pathway that controls trichome initiation (Hülskamp and Schnittger, 1998; Hülskamp, 2004). The active WD40-bHLH-MYB complex activates trichome differentiation by directly inducing the expression of a homeodomain-leucine zipper (HD-ZIP) IV gene GLABRA2 (GL2) (Schellmann and Hülskamp 2005). Although it is possible that the regulation pathway of unicellular trichomes is different from that of multicellular trichome, many regulatory factors have the same
effect under different regulation pathways. For instance, Over-expression of \textit{CsTRY}, \textit{PaTRY}, \textit{PaCPC-like1}, \textit{PaCPC-like2} and \textit{PaCPC-like3} in \textit{Arabidopsis} resulted in glabrous phenotype (Tang et al., 2012; Zhang et al., 2019). \textit{CsGL3}, \textit{CsGL1}, \textit{MICT} (Micro-trichome), \textit{TBH} (Tiny branched hair), and \textit{TRIL} (Trichome-less) encode HD-Zip proteins with different subfamilies; genetic and molecular analyses have revealed that these transcription factors are responsible for the differentiation of epidermal cells and the development of multicellular trichomes in cucumber (Liu et al., 2016). Though qRT-PCR analysis of trichome-related genes in different organs which covered with different types trichomes, we found that most of these trichome-related genes showed broadly consistent patterns of expression in RR and RS. This observation may partly explain the different types trichome in different organs. Based on the expression of trichome-related genes in different organs with different types of trichomes in RR and RS, we have proposed that there are differences in the regulation of trichomes between these two germplasms. Our results indicate that \textit{GL1} and \textit{GL2} affect acicular trichome development in RR and RS, and that \textit{TTG1} and \textit{TRY} acts only in RR. The described regulatory changes may cause the abundance of acicular trichomes and glandular trichomes in RS, and the repression of some trichome-related genes. The \textit{PDF2} of \textit{Arabidopsis} has not been shown to be involved in trichome formation but type I trichome formation is controlled by \textit{PDF2} in tomato (Yang et al., 2011). However, the expression of \textit{PDF2-like} was higher in the pedicel and pericarp, which were covered with glandular trichomes; such diverse expression patterns suggest that \textit{PDF2-like} may be regulating glandular trichomes in RS and a different regulatory pathway occurs in RR. \textit{CPC} plays an important role in the regulation of non-glandular and glandular trichomes, as indicated in plant species including tomato, poplar, and London plane (Tominaga-Wada et al., 2013; Zhang et al., 2019). However, here the expression level of \textit{CPC} in tissues without glandular trichomes are significantly higher than those with. This finding suggested that \textit{CPC} mainly regulates the formation of glandular trichomes in RR and RS.
During three stages of bud and seven stages of floral bud development, all these genes responded to the growth stages, thereby potentially eliciting influence on trichome initiation. However, the expression patterns were inconsistent between RR and RS. In this study, we found maximum expression of GL1, GL3, TTG1, PDF2, CPC and TRY at the Fb3 stage of floral bud development in RR, but all of these genes had the highest expression at the B3 stage of bud development in RS. Since different types of trichomes were present in RR compared to RS, we reasoned that the Fb3 stage is a critical trichome developmental period of RR, whereas the B3 stage is for RS. The transcripts of GL1, GL2, GL3, PDF2-like and CPC were expressed highest in the B3 stage of bud and floral bud development in RS, which may be due to the range of developmental stages of buds, and how the glandular and acicular trichomes were clustered on newly growing shoots and leaves. We observed that most trichome related genes have only one peak in Fb3 of floral bud development of RR, whereas the GL1, GL2 and TRY had three peaks in Fb1, Fb3 and Fb5. This may suggest that these genes play vital roles in acicular trichome development and formation in floral buds of RR. These trichome-related genes are highly expressed in young leaf primordia and then progressively decrease as trichomes begin to initiate (Kirik et al., 2005). However, here the expression of these genes peaked at different developmental stages in different organs and correlated with the formation of different types of trichome, suggesting not only a role in trichome initiation, but also formation.

The types, distribution and micromorphology of trichomes in RR and RS were studied and putative regulatory genes identified. The data presented here provides a basis for creating new Rosa varieties with desired trichome growth and density through breeding and genetic engineering and helps to understand the complex network of regulatory interactions controlling the development of multicellular trichomes. This is the first report of quantitative analysis of trichome-related gene expression during bud development across different
trichomes types and organs. Future work should focus on validating a set of reference genes related to trichome initiation and growth, and to determine the precise function of these genes in *Rosa*.

**Acknowledgements**

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**References**


Rosa roxburghii. Hortscience. 54, 45-51.


FIGURES:

Fig.1 The sampling site of R. roxburghii Tratt. (A, D, F, H) and R. sterilis S. D. Shi (B, C, E, G, I) for RNA extraction. (a) Sarcocarp; (b) Pericarp; (c) Pedicel; (d) Bearing branch; (e) Vein; (f) Mesophyll; (g) Sepal I; (h) Sepal II.
Fig. 2. The macroscopic depiction of *R. roxburghii* Tratt. (A-E) and *R. sterilis* S. D. Shi (F-K) organs. (A) Floral bud; (B) Ripe fruit; (C) Stem; (D) Leaf abaxial; (E) Leaf adaxial; (F) Floral bud; (G) Ripe fruit; (H) Immature stem; (I) Stem; (J) Leaf abaxial; (K) Leaf adaxial.
Fig. 3. SEM of trichomes of *R. roxburghii* Tratt. and *R. sterilis* S. D. Shi (A) flagellate trichomes (stars) and acicular trichomes (white arrows) on immature sepals of *Rosa roxburghii* Tratt.; (B-D) Trichomes on immature sepals of *Rosa sterilis* S. D. Shi. (B) Capitate glandular trichomes (black arrows) and acicular trichomes (white arrows); (C) Branch trichomes; (D) Flagellate trichomes (stars); (E) Acicular trichomes (white arrows) on immature pericarp of RR; (F-H) Trichomes on immature pericarp of RS; (F) Acicular trichomes (white arrows) and capitate glandular trichomes (black arrows); (G) Capitate glandular trichomes with an obvious stoma (drawing districts) on the top of glandular head; (H) Acicular trichomes local magnification map; (I) Trichomes on immature pedicel of RR; (J-K) Trichomes on immature pedicel of RS; (J) Capitate glandular trichomes (black arrows); (K) Capitate glandular trichomes local magnification map; (L) Bearing branch of RR; (M) Bearing branch of RS with flagellate trichomes (stars); (N) Immature stem of RR; (O-Q) Immature stem of RS; (O) Capitate glandular trichomes (black arrows); (P) Capitate glandular trichomes local magnification map; (Q) Bowl-shaped glandular trichomes.

Fig. 4. Development of trichomes of *R. roxburghii* Tratt. (A-C) and *R. sterilis* S. D. Shi (D-G). (A) Acicular trichomes (white arrow) on floral bud; (B) Acicular trichomes (white arrow) on fruit; (C) Acicular trichomes (white arrow) on younger pedicel; (D) Capitate glandular trichomes (black arrow) and acicular trichomes (white arrow) on floral bud; (E) Capitate glandular trichomes (black arrow) and acicular trichomes (white arrow) on fruit; (F) Capitate glandular trichomes (black arrow) and flagellate
trichomes (stars) on younger pedicel; (G) Capitate glandular trichomes (black arrow) and acicular trichomes (white arrow) on mature pedicel.

Fig. 5. Light microscopy images of acicular trichomes and prickles of *R. roxburghii* Tratt. (A-C) and *R. sterilis* S. D. Shi (D-F) (A) Acicular trichomes (white arrows) on the fruit; (B) Acicular trichomes (white arrows) on the pedicel; (C) Prickle on the stem; (D) Acicular trichomes (white arrows) on the fruit; (E) Capitate glandular trichomes (black arrows) on younger pedicel; (F) Prickle on the stem (RAZ: resembling abscission zone).
Fig. 6. Transmission electronic microscopic images of acicular trichomes of *R. roxburghii* Tratt. (A-D) and *R. sterilis* S. D. Shi (E-H). (A) Acicular trichomes of sepals; (B) A local magnification map; (C) Acicular trichomes on fruit; (D) C local magnification map; (E) Acicular trichomes of sepals; (F) E local magnification map; (G) Acicular trichomes on fruit; (H) G local magnification map. N: Nucleus; CW: cell wall; V: vacuole; GA: Golgi body; M: Mitochondria.

Fig. 7. Sepals with flagellate trichomes of *Rosa roxburghii* Tratt. (A-B) and *Rosa sterilis* S. D. Shi (C-D) viewed by transmission electronic microscopic. Dense thready material (arrow) N: Nucleus; CW: cell wall; V: vacuole; SG: starch grains.

Fig. 8. Transmission electronic microscopic images of young prickles of *Rosa roxburghii* Tratt. (A-B) and *Rosa sterilis* S. D. Shi (C-D). CW: cell wall; V: vacuole.
Fig. 9. Ultrastructure of the head of the capitate glandular trichomes in *Rosa. sterilis* S. D. Shi (A) Capitate glandular trichomes of sepals; (B-C) A local magnification map (arrow indicates stained secretory product); (D) Capitate glandular trichomes of pedicel (arrow indicates stained secretory product); (E-F) D local magnification map (arrow indicate stained secretory product); (G) Capitate glandular trichomes of fruits; (H-I) G local magnification map; (J) Capitate glandular trichomes of stems (arrow indicates stained secretory product); (K-L) J local magnification map (arrow indicates dense granular material) N: Nucleus; CW: cell wall; ICS: intercellular spaces; V: vacuole; SG: starch grains.
Fig. 10. Fourier transform infrared spectra of prickles of fruit and stem in RR and RS. (A) Fourier transform infrared spectra of prickles on fruit in *Rosa roxburghii* Tratt. and *Rosa sterilis* S. D. Shi; (B) A Partial enlargement map; (C) Fourier transform infrared spectra of prickles on stem in RR and RS; (D) C Partial enlargement map.
Fig. 11. DNA ploidy analysis of *Rosa sterilis* S. D. Shi and *Rosa roxburghii* Tratt. (A) DNA ploidy map of leaves in RS, (B) DNA ploidy map of fruit prickles in RS, (C) DNA ploidy map of leaves in RR, (D) DNA ploidy map of fruit prickles in RR.
Fig. 12. qRT-PCR analysis of genes related to trichome development in different parts of *R. roxburghii* Tratt. (A, C, E, G) and *R. sterilis* S. D. Shiat (B, D, F, H). Values are expressed as the means of at least three independent replicates ± SD. * = significant to p < 0.05.
**Fig.13.** Expression pattern of trichome formation related genes in bud and floral bud of *R. roxburghii* Tratt. and *R. sterilis* S. D. Shi at different development stages. Values are expressed as the means of at least three independent replicates ± SD. Note: B: buds; Fb: flora buds.
Table 1: qRT-PCR primer information of related genes

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<tr>
<th>Gene name</th>
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<th>Gene name</th>
<th>Primer sequence 5'-3'</th>
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<td>GL1</td>
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<td>PDF2</td>
<td>Forward: ACATGCTGCTTACGATGACCTCAC</td>
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<td>Reverse: CCAACACTAATCCTGACTGATCC</td>
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<td>Reverse: AGACTCTGAGATGCTACTCAACTG</td>
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<td></td>
<td>Reverse: CAACAGGACAGCATCATGTTTATC</td>
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<td>Reverse: TTCTCCCTCTATCTGAGACCA</td>
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<tr>
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<td>CPC</td>
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<td></td>
<td>Reverse: TCACGTATTAGGACGGAGAC</td>
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<td>Reverse: GGAAGATCGACAGGAGATGAG</td>
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<td>TRY</td>
<td>Forward: TTAAGGCAAGTGAAGCATATGG</td>
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<td></td>
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<td></td>
<td>Reverse: ACGACTCGGATGTGTCATATCC</td>
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<td>UBQ</td>
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Note: "—" showed absent; values are means ± SD (n=30), different small letters in the same column meant significant difference at P < 0.05 levels respectively.

Table 2: The trichome types, distribution and characteristics (mean ± SE) of *R. roxburghii* Tratt. and *R. sterilis* S. D. Shi

<table>
<thead>
<tr>
<th>Species</th>
<th>Organ</th>
<th>Non-glandular trichome</th>
<th>Glandular trichome</th>
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</thead>
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<tr>
<td></td>
<td></td>
<td>Flagellate trichomes (µm)</td>
<td>Acicular trichomes (µm)</td>
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<td><em>Rosa roxburghii</em></td>
<td>Sepal</td>
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<td>499.8±148.34c</td>
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<td>—</td>
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<tr>
<td></td>
<td>Pedicel</td>
<td>208.5±40.44c</td>
<td>841.2±67.42b</td>
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<td>Tratt.(RR)</td>
<td>Bearing branch</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>Stem</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>Leaf adaxial</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>Leaf abaxial</td>
<td>—</td>
<td>443±65.15cd</td>
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<tr>
<td><em>Rosa sterilis</em></td>
<td>Sepal</td>
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<td>489.5±167.68c</td>
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<tr>
<td></td>
<td>Pericarp</td>
<td>—</td>
<td>577.2±149.01c</td>
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<tr>
<td>S. D. Shi (RS)</td>
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<td>451.2±112.51a</td>
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<td></td>
<td>Bearing branch</td>
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<td>3185.3±95.32b</td>
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<tr>
<td></td>
<td>Leaf abaxial</td>
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