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Dissecting a Hidden Gene Duplication: The Arabidopsis thaliana SEC10 Locus

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Abstract
Repetitive sequences present a challenge for genome sequence assembly, and highly similar segmental duplications may disappear from assembled genome sequences. Having found a surprising lack of observable phenotypic deviations and non-Mendelian segregation in Arabidopsis thaliana mutants in SEC10, a gene encoding a core subunit of the exocyst tethering complex, we examined whether this could be explained by a hidden gene duplication. Re-sequencing and manual assembly of the Arabidopsis thaliana SEC10 (At5g12370) locus revealed that this locus, comprising a single gene in the reference genome assembly, indeed contains two paralogous genes in tandem, SEC10a and SEC10b, and that a sequence segment of 7 kb in length is missing from the reference genome sequence. Differences between the two paralogs are concentrated in non-coding regions, while the predicted protein sequences exhibit 99% identity, differing only by substitution of five amino acid residues and an indel of four residues. Both SEC10 genes are expressed, although varying transcript levels suggest differential regulation. Homozygous T-DNA insertion mutants in either paralog exhibit a wild-type phenotype, consistent with proposed extensive functional redundancy of the two genes. By these observations we demonstrate that recently duplicated genes may remain hidden even in well-characterized genomes, such as that of A. thaliana. Moreover, we show that the use of the existing A. thaliana reference genome sequence as a guide for sequence assembly of new Arabidopsis accessions or related species has at least in some cases led to error propagation.

Introduction
Evolution of plant genomes frequently involves segmental and even whole-genome duplication events. Gene duplications provide a crucial source of raw material for evolution of organisms [1]. Upon fixation, the evolutionary fate of gene duplications can follow a few different scenarios: conservation of gene function, pseudogenization, subfunctionalization or neofunctionalization (reviewed in [2–4]). The fate of duplicated genes, resulting from an interplay of chance and selection, appears to correlate with their function, as well as their mode or history of duplications. Gene duplicates within certain functional categories are retained or lost with varying probability in flowering plants [5,6], and products of whole genome duplications behave differently from those resulting from single gene tandem duplications [7].

The nuclear genome of Arabidopsis thaliana, one of the smallest genomes among land plants, and undoubtedly the best characterized one, contains over 27,400 protein-coding genes (see TAIR — http://www.arabidopsis.org and [8]) and exhibits a significantly higher fraction (37%) of predicted genes belonging to gene families with more than five members, compared to organisms with a similar number of genes — Drosophila melanogaster (12%) or Caenorhabditis elegans (24%), reflecting more abundant gene duplications [9]. This phenomenon may be explained, e.g., by more relaxed constraints on the genome size in plants, by a more prominent role of unequal crossing-over to generate new gene copies [9], or by a selective advantage of subtle functional tuning, or subfunctionalization, contributing to the survival of paralogous genes in sessile organisms as adaptation to unavoidable occasional adversity of local conditions [3].

The Arabidopsis thaliana genome sequencing project engaged the strategy of hierarchical or clone-by-clone sequencing [9]. In essence, the genome was first broken into large fragments that were subsequently cloned into BACs (Bacterial Artificial Chromosomes) in order to obtain a genomic library. Afterwards, each BAC was read using the shotgun sequencing method, employing another round of fragmentation and Sanger sequencing. All reads were then computationally assembled to create contiguous sequences corresponding to BACs and to original chromosomes. The assembly step has long been known as a possible source of errors in genome sequence reconstruction, especially in the case of highly identical repetitive sequences longer than an average read.
length [10,11]. While this problem has been recognized in human and rodent genome assemblies [12–15] and partly overcome by more advanced algorithms, such as ARACHNE [16] or PCAP [17], as well as by “next generation” assembly algorithms developed in parallel with the new high-throughput mass parallel sequencing techniques (reviewed in [10]), the bulk of the current “gold standard” A. thaliana genome assembly predates these methodological improvements. While occasional corrections are being introduced regularly in the process of genome updating and re-annotation, they currently, as a rule, concern only point mutations and short (several bp) indels spanned by cDNA or EST (Expressed Sequence Tag) sequences [19].

The availability of A. thaliana genome sequence opened a gate towards complete inventories of evolutionarily conserved genes. We have previously used sequence information to find homologs of all subunits of the exocyst complex in Arabidopsis [20–23]. This hetero-octameric protein complex, consisting of Sec3, Sec5, Sec6, Sec8, Sec10, Sec15, Exo70, and Exo84 subunits, functions in the last steps of exocytosis – in docking and tethering of secretory vesicles to the plasma membrane (reviewed in [24,25]). Genes encoding all eight exocyst subunits were also found in all land plants examined, often forming families of paralogs, which is in contrast to the situation in yeast or metazoan, where each subunit is encoded by a single gene or (in vertebrates) small families of paralogs [23]. A. thaliana has two Sec3, Sec5 and Sec15 paralogs, three Exo84 paralogs, and 23 Exo70 paralogs, a number unparalleled outside the plant kingdom [21–23,26]. The remaining three subunits, Sec6, Sec8, and Sec10, are each encoded by a single gene according to the current genome annotation.

Here, we report that the SEC10 exocyst subunit in A. thaliana is in fact encoded by two genes in tandem, and that 7 kb of sequence at the SEC10 locus (At5g12370) is missing in the A. thaliana reference genome assembly. This demonstrates that assembly errors involving highly similar sequences in tandem duplication may lead to genome sequence artifacts and omission of functional genes even in a well characterized genome such as that of A. thaliana. We also document here that the two SEC10 genes are most probably functionally redundant in plant cells.

**Results**

Different lines of evidence hint for the presence of two copies of the SEC10 gene in the A. thaliana genome

A single gene (At5g12370) coding for the SEC10 exocyst subunit was previously identified in the genome of Arabidopsis thaliana [21]. However, two independent lines of evidence led us to suspect that the At5g12370 locus may have been incorrectly assembled during the genome sequencing due to a tandem gene duplication, and that at least two genes encoding SEC10 are present in the A. thaliana genome.

First, a SEC10 cDNA sequence [GenBank: AF479280] that we obtained by sequencing a cDNA clone identified on the basis of partial EST sequence data [GenBank: AV528809] [27] exhibited multiple single nucleotide mismatches compared to any of the alternative reference TAM10) SEC10 cDNA sequences predicted on the basis of genomic data [GenBank: NM_121275.4]; alternative predictions [GenBank: NM_001036794.1; GenBank: NM_001036795.2] are not considered further for simplicity. The same discrepancy with the reference sequence was also evident in a cDNA sequence [GenBank: AY096638] originating from a large-scale cDNA sequencing project [28]. The coding sequences of AF479280 and AY096638 are identical (except a single substitution in AY096638 most likely reflecting a sequencing error), and are furthermore identical to the coding sequence of a SEC10 gene that we previously obtained by RT-PCR (Reverse Transcription PCR) from A. thaliana Col-0 seedlings [29]. Parts of the untranslated regions (UTR) flanking the coding sequences of AF479280 and AY096638 are also identical, although the very 5’ and 3’ extremities of the two cDNAs differ (see below). When compared to the reference cDNA sequence (NM_121275.4), both AF479280 and AY096638 exhibit 27 single nucleotide differences in 12 out of 24 coding exons, whereas the remaining coding exons are identical (overall sequence identity within the coding sequence is thus over 99%). In addition, an extra 12-bp-long sequence is present within exon number 16 of AF479280 and AY096638, and is without a counterpart in the reference genome sequence. On the other hand, using BLAST, we found another SEC10 cDNA [GenBank: AK222187] from a large-scale cDNA sequencing project [30], which does match perfectly the reference cDNA sequence [GenBank: NM_121275] except for the last 72 bp of the 3’ UTR, which do not align with the reference cDNA at all and have no corresponding sequence even in the genome assembly, raising thus the possibility of a cloning artifact.

Second, in several Arabidopsis mutant lines with T-DNA insertions in SEC10, the offspring of self-crossed putative heterozygous plants, which were fully fertile, exhibited a confusing segregation ratio of 1:3:0 or 0:1:0 (w/w : w/m : m/m) when analyzed by PCR genotyping (Table S1). This could not be explained by embryonic or gametophytic lethality, and therefore, we speculated that a PCR product corresponding to the wild-type allele might be amplified from another (yet unknown) very similar SEC10 paralog present in the genome. We proposed that the apparent heterozygotes in the populations segregating were, in fact, a mixture of genuine heterozygotes and homozygotes that exhibited a wild-type signal from another SEC10 paralog in PCR genotyping. In the latter case (0:1:0), the assumed heterozygous parent plants were most likely homozygous plants in fact. If this was the case, and homozygous plants were present in the offspring, no obvious mutant phenotype was noticed. This is notably unlike mutants in the two other exocyst subunits encoded by a single gene, as SEC6 and SEC8 exhibit pollen-specific transmission defects of mutant alleles [29,31]. This suggested that the function of the disrupted gene might be complemented by an unknown second gene also encoding a SEC10 subunit of the exocyst complex.

Re-sequencing of the SEC10 locus reveals the presence of tandemly duplicated SEC10 genes

Few gaps are known to remain in the A. thaliana reference genome sequence, most of them in centromeres and pericentromeres [http://www.arabidopsis.org/portal/gen/annotation/gene_structural_ annotation/agicomplete.jsp]. If the hypothetical second SEC10 copy does not reside in a gap, it would be most likely located at the SEC10 locus itself, and its absence from the reference genome sequence may be due to an assembly artifact caused by collapsing a tandem duplication of the SEC10 gene into one copy.

To test this hypothesis, we designed a pair of outward-facing PCR primers, A and B (Figure 1A; Table S2), matching the first and the last exon, respectively, of the SEC10 gene in regions that are identical in the two different SEC10 cDNA versions. Depending on the presence and orientation of another SEC10 version(s), PCR reactions using primer A only, primer B only, or both primers together on genomic DNA template should yield products allowing us to distinguish between the possible locus arrangements (Figure 1A). Indeed, using genomic DNA from the Columbia-0 (Col-0) ecotype as a template, we obtained a PCR product only with the combination of A and B primers. This
product corresponds to the presumed intergenic region between the hypothetical tandemly duplicated SEC10 genes in the “head to tail” orientation (Figure 1B). The same product was obtained also on templates from two other A. thaliana ecotypes, Landsberg erecta (Ler-0) and Nossen (No-0) (Figure S1A), indicating that the gene duplication is not restricted to the Col-0 ecotype. In contrast, a similar experiment with Arabidopsis lyrata using species-specific primers showed no duplication in this species (Figure S1B). To distinguish the two SEC10 genes in A. thaliana, we labeled the upstream gene (in the direction of transcription) as SEC10a and the downstream gene as SEC10b (Figure 2).

The PCR product obtained from Col-0 DNA was cloned and sequenced, providing an intergenic sequence of 1511 bp between the stop codon of SEC10a and the start codon of SEC10b. The first 108 nucleotides at the 5’ end of the intergenic sequence (i.e., downstream of the stop codon of the SEC10a gene) were identical to the region of the reference genome sequence immediately downstream of the sole SEC10 gene [A. thaliana chromosome 5 [GenBank: CP002688.1], positions 4002894-4003001 in the complementary strand, but the rest of the amplified segment could not be matched perfectly to the reference genome sequence (Data S1). Thus, nearly the complete intergenic region between the SEC10a and SEC10b genes, and the whole coding sequence of the SEC10b gene, are missing from the current reference genome sequence of A. thaliana.

Using the newly determined intergenic sequence and sequences of the genes flanking the SEC10 locus, we designed specific primers to amplify and clone both SEC10 versions present in the A. thaliana Col-0 genome. As we were unable to amplify whole SEC10 genes, probably due to their length of approx. 9 kb, we cloned each SEC10 gene in two halves using additional primers designed on the basis of the known cDNA sequences of both SEC10 versions and matching internal exons conserved between the two SEC10 genes (Figure 2). Four overlapping PCR products covering the entire SEC10 locus were obtained, cloned and sequenced. Finally, a complete sequence of the SEC10 locus was manually assembled [ENA: HG764169].

Comparison of our assembled sequence, including the SEC10 tandem duplication, with the reference genome sequence revealed that a 7 kb sequence segment is missing from the reference (Figure S2). Because the artificial deletion occurs in a duplicated region, its position with respect to the current sequence of the chromosome 5 [GenBank: CP002688.1] cannot be unambiguously defined. We arbitrarily define the position of the deletion between the nucleotides 4002893 and 4002894 of the current assembly of the chromosome 5, in which case the deleted region comprises (in the direction identical with the orientation of the two SEC10 genes) a part of the 3’ UTR region of the SEC10a (corresponding to the AK222187 cDNA, see above), the putative promoter region of the SEC10b gene, and nearly the whole SEC10b itself, except the very terminus of its 3’ UTR (Figure 2 and S2). This means that the SEC10b gene sequence in the reference genome assembly is a chimera consisting primarily from SEC10a, except a region in its 3’ UTR derived from SEC10b. We therefore suggest that the systematic gene ID assigned to the original misassembled SEC10 gene, At5g12370, should be used to designate the SEC10a gene, whereas the SEC10b gene could be designated with a new ID, At5g12365.

A comparison of the SEC10a and SEC10b sequences (their alignment in Data S1) revealed regions of discernible homology both upstream of the CDS (including a putative promoter and the transcribed 5’ UTR) and downstream of the CDS (the 3’ UTR and a region downstream of the polyadenylation site). The first fifth and the last sixth of the sequence between the start and stop codons is identical with an exception of four substitutions. There are at least 40 indels between the two paralogs, ranging from 1 to 35 nucleotides. All but one are located in the non-coding regions. The indel in the coding sequence occurs in the 16th coding exon and accounts for twelve nucleotides. The identity of coding exons ranges between 95% and 100%, whereas the identity of introns ranges between 79% and 100% (ignoring indels longer than one nucleotide). A comparison of the A. thaliana SEC10 genes with the sole A. lyrata homolog revealed that AtSEC10a and AtSEC10b are mutually more similar than any of them to A. lyrata SEC10 (Data S2), suggesting that the duplication occurred after the divergence of the A. lyrata and A. thaliana lineages. This comparison also suggests that the twelve-nucleotide indel in the coding sequences of SEC10a and SEC10b is due to a deletion in SEC10a rather than an insertion in SEC10b.

Differences in the predicted protein sequences of the two SEC10 paralogs are minor, since most of the substitutions in exons are silent. The SEC10a and SEC10b proteins differ only by substitution of five amino acid residues (G4R, A235T, V500F, D503E, T679P), in addition to a deletion of four amino acid residues (TSVS at position 569) in the SEC10a protein (Figure S5). This high degree of similarity suggests that SEC10a and SEC10b isoforms might be functionally redundant.

Both SEC10 gene copies are expressed in A. thaliana, yet SEC10b is the dominant isoform

Using our complete sequence of the SEC10 locus, we could explain the differences in the various SEC10 cDNA sequences

![Figure 1. Evidence for SEC10 gene tandem duplication. (A) Expected outcomes of diagnostic PCR with outward-facing primers “A” and “B” (gray and black arrows), specific to each end of the SEC10 gene, for potential structures of the SEC10 locus (a single gene or three variants of tandem gene duplication). The table on the right shows the expected presence or absence (+ or -) of PCR products using different primer combinations. (B) Results of PCR reactions according to (A) using A. thaliana Col-0 genomic DNA as a template. doi:10.1371/journal.pone.0094077.g001](image-url)
obtained by us or others (see above and Table S2). Thus, the cDNA AK222187 [30] could be unambiguously assigned to SEC10a, whereas the cDNAs AF479280 and AY096638 [28] match perfectly the SEC10b gene. The differences in the 5′ and 3′ UTRs of AF479280 and AY096638 most likely result from an alternative transcription initiation and polyadenylation, with the transcription start for the AY096638 sequence located within the region corresponding to the second intron as defined by the AF479280 sequence and with polyadenylation starting downstream of that in AF479280.

Earlier, we amplified the coding sequence of the SEC10b cDNA using a total cDNA prepared from Col-0 seedlings [29]. However, repeated attempts to amplify the coding sequence of SEC10a from cDNA templates prepared from various tissues and stages of Col-0 using primers that would amplify both SEC10a and SEC10b yielded only additional SEC10b clones (40 clones tested in total), as determined by restriction analysis of cloning and polyadenylation, with the transcription start for the SEC10a gene, albeit the existence of the AK222187 cDNA [30] proves that it indeed is expressed. We then used cDNA prepared from sec10b-1 homozygous T-DNA insertion mutants (SALK_120710) as a template. Two types of PCR products of slightly different size were cloned (Figure S4B). The longer ones match perfectly the SEC10a transcript on human genome sequence based on clone-by-clone sequencing or whole-genome shotgun sequencing (WGS), respectively, revealed serious errors in the reference genome sequence of rice caused by assembling of repetitive sequences were identified recently [34]. Importantly, comparison of two independent assemblies of the human genome sequence based on clone-by-clone sequencing or whole-genome shotgun sequencing (WGS), respectively, revealed an apparently higher frequency of SEC10b clones in wild-type plants. We conclude that both SEC10a and SEC10b are functional genes that are expressed in A. thaliana.

**Analysis of insertional mutants indicates a functional redundancy of SEC10a and SEC10b**

Using the revised sequence of the SEC10 locus, we designed paralog-specific sets of primers for PCR genotyping and performed new segregation analyses of selected T-DNA insertional mutant lines in both SEC10a and SEC10b (Figure 3A). For each line, we performed sequencing of the region flanking the Left border of the T-DNA to determine whether the T-DNA is inserted in SEC10a or SEC10b (flanking sequences provided by the collections were usually insufficiently long with respect to high similarity between SEC10a and SEC10b). Semi-quantitative RT-PCR showed that all mutant lines are null alleles, expressing no detectable specific mRNA; whereas transcripts from the unaffected paralog were detected in all cases (Figure 4B). The segregation ratio in all mutant lines was compatible with Mendelian rules (1:2:1) (Table 1) and a phenotype analysis of sec10a and sec10b homozygous mutants revealed no observable deviations from wild-type plants. Thus, we suggest that both genes share overlapping functions and exhibit redundancy under standard culture conditions.

**Discussion**

Repetitive sequences, including gene duplications, present a major source of computational difficulties for genome sequence assembly and mapping based on shotgun sequencing approaches. Serious errors in the reference genome sequence of rice caused by assembling of repetitive sequences were identified recently [34]. Importantly, comparison of two independent assemblies of the human genome sequence based on clone-by-clone sequencing or whole-genome shotgun sequencing (WGS), respectively, revealed an apparently higher frequency of SEC10b clones in wild-type plants. We conclude that both SEC10a and SEC10b are functional genes that are expressed in A. thaliana.

**Figure 2. The revisited structure of the SEC10 locus in Arabidopsis thaliana.** The revisited arrangement of the SEC10 locus (At5g12370) depicts SEC10a, SEC10b, and parts of two neighboring genes (At5g12360, At5g12380). Coding exons are shown as black boxes, 5′UTR as gray boxes, and 3′ UTR as white boxes. Arrows indicate the position and orientation of primers used for cloning of the SEC10 locus in four overlapping parts (a-I, a-II, b-I and b-II; lines at the bottom represent the regions of the cloned PCR products). The orange strip marks the region omitted from the reference sequence of the A. thaliana genome.

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**Figure 3. Expression levels of SEC10a and SEC10b in various tissues of A. thaliana.** (A) Specificity of the PCR primers demonstrated on paralog-specific cDNAs (AK222187 for SEC10a and AY096638 for SEC10b, indicated above the line), using primer sets specific for SEC10a or SEC10b (indicated below the line as a or b, respectively). (B) Expression levels of SEC10a and SEC10b in various tissues as analyzed by semi-quantitative RT-PCR. The expression level of the ACT7 gene was used as a control.

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that at 95.5% or greater sequence identity large segmental duplications disappear from the WGS assembly [14]. It is estimated that 50%–60% of highly similar (>90%) segmental duplications are not resolved as duplicated copies within the WGS assemblies of human, mouse and rat genome sequences [35]. At >97% identity, the portion of unresolved duplications increases up to 91% as calculated in She et al. [14]. For example, single-nucleotide polymorphisms interpreted in databases as different alleles could often be potential paralogous sequence variants, depending on the threshold set in the assembling software [13]. Assembling the shotgun reads from individual clones cases the task because duplications are often split into different non-overlapping clones. Therefore, the clone-by-clone sequencing approach is superior to WGS in the resolution of segmental duplications [14]. Although clone-by-clone sequencing was employed in the A. thaliana genome sequencing project [9], the computational sequence assembly of individual clones (BACs, ~200 kb) is still largely sensitive to within-clone near-identical segmental duplications (especially when in tandem), albeit the complexity of sequences assembled from shotgun data is relatively low. Reassembling of the Arabidopsis genome sequence from the original reads using the latest software would be advisable to uncover at least a portion of hidden gene duplications. Alternatively, remapping of the original reads to the genomic sequence assembly and subsequent analysis of regions that exhibit an excessive read coverage may detect sites of potential duplication that would be further inspected manually [14,36].

In case of the A. thaliana SEC10 gene, the history of reference sequence updates did not suggest an assembly problem. Although the whole locus was missing (i.e. located within a gap) in the original genome sequence release ([9], GenBank: NC_003076_1), its reference sequence went unchanged since it appeared in the first revision of the Chromosome V reference sequence in 2001 (GenBank: NC_003076_2). However, we noticed the existence of cDNA sequences incompatible with the reference genome sequence (already mentioned in [23]), and obtained suspicious results from genotyping insertional mutants in the SEC10 gene, which prompted us to re-sequence the whole SEC10 locus. Since only one PCR product was amplified in a reaction employing outward-facing primers (Figure 1), we concluded that a single tandem repeat of SEC10 gene is probably present in the genome (unless the intergenic regions between the potential additional SEC10 copies have an identical length). Subsequent subcloning and sequencing with manual assembly revealed that the locus indeed harbours two copies of the SEC10 gene, similar enough to be collapsed into one chimeric locus by assembly algorithms. As a result, 7 kb were omitted from the final genome sequence, apparently due to an error during the sequence assembly of the BAC clone T2L20 [ENA: AL592312.1] that represents the region including the SEC10 locus in the A. thaliana chromosome 5 pseudomolecule. We attempted to obtain the original raw sequencing reads for the T2L20 clone, but unfortunately they have not been retained after the completion of the Arabidopsis genome project (Mike Bevan, John Innes Centre, Norwich, UK, personal communication), so we could not directly revisit the assembly of the T2L20 sequence and had to employ the strategy based on PCR amplification of the misassembled SEC10 locus.

Since the A. thaliana reference genome sequence has been used as a framework for sequence assembly in numerous additional sequencing projects aimed at characterizing Arabidopsis genome diversity, the omission of one of the two SEC10 genes may have been propagated into additional sequencing projects. In particular, the Ler-0 genome sequence [37], as well as Bur-0, C24 and Kro-0 ecotypes accessible at the website [http://www.1001genomes.org](http://www.1001genomes.org)
of the “1001 genomes” project [38], contains a single SEC10 gene, even though our PCR-based test indicates the presence of two SEC10 copies in Ler-0, similar to the Col-0 ecotype. However, somewhat encouragingly, the SEC10 protein prediction is missing in several of the 19 predicted proteomes derived from the first phase of the “1001 genomes” study (available at http://mus.well.ox.ac.uk/19genomes/), including No-0, another accession shown here to carry the duplication. Thus, although the error propagation problem in reference-guided genome assemblies undoubtedly exists, it might be to some extent self-limiting, since gene duplications may result in assembly problems leading to exclusion of problematic sequence areas from further processing. Encouragingly, a BLAST search of the recently released Pacific Biosciences Ler-0 genome sequence (available at http://www.pach.com/devnet/) that was obtained by de novo assembly using a novel HGAP algorithm with improved ability to resolve long repeats [39], revealed the presence of a complete duplicated SEC10 locus, with hits of over 98% nucleotide sequence identity covering 97% of the 18-kb sequence segment we submitted to ENA, independently confirming our observations.

We confirmed that both SEC10 isoforms are expressed, as already indicated by existing cDNA sequences corresponding to both versions, albeit both the public sequence data and our observations document higher expression of the SEC10b paralog. Publicly available microarray data from the Genevestigator database, obtained using the ATH1 Affymetrix DNA chip show constitutive SEC10 expression in all Arabidopsis tissues and stages [40]. Nevertheless, the specificity of eleven 25-bp-probes (245211_at) on the ATH1 chip referring to the “single-copy” SEC10 gene is uncertain, because they probably recognize both SEC10 paralogs – all probes have full identity to SEC10b, whereas seven probes match fully and four probes match each with one mismatch the SEC10b sequence. Thus, analyses of promoter specificity and protein localization using reporter genes will be necessary to investigate paralog-specific SEC10 expression patterns. Without such data, covering preferentially multiple ecotypes or species, we can only speculate whether the apparent under-representation of the SEC10a transcript under standard culture conditions reflects distinct environmental regulation of the two copies, restriction of the SEC10a expression to some minority cell type(s), or even ongoing pseudogenization of this paralog.

The lack of observable phenotypic deviations in single mutants favors a hypothesis that the two genes exhibit mostly overlapping expression patterns in Arabidopsis tissues and are to a large extent functionally redundant, although SEC10b is apparently more abundantly expressed based on our semi-quantitative RT-PCR experiments with paralog-specific primers (Figure 3), as well as on the failure to amplify the SEC10a transcripts in RT-PCR with paralog-indiscriminating primers. A similar situation has been documented for SEC5a and SEC5b duplicated genes, coding for another exocyst subunit, where SEC5a has considerably higher expression than SEC5b, although otherwise showing a similar expression pattern (data from Genevestigator; [40]). The expression of SEC5b only in sec5a mutants is sufficient for cellular functions, and a mutant phenotype is apparent only in sec5a sec5b double mutants, which could be obtained by recombination, given that the two SEC5 copies reside on different chromosome arms [29]. However, in the case of the tandemly arranged SEC10a and SEC10b, double mutants would be extremely difficult to obtain, due to the extremely restricted space for recombination between the two genes. Our analysis of SEC10a/SEC10b expression in whole seedlings and three entire organs, however, does not exclude the possibility of paralog-specific expression patterns in particular cell types or tissues. Such differences in paralog expression have been indeed found for several pairs of duplicated genes encoding exocyst subunits – e.g. SEC15a and SEC15b, EXO70A1 and EXO70A2, or EXO70H3 and EXO70H4 (data from Genevestigator [22,40]).

The likely functional redundancy of SEC10a and SEC10b is supported also by comparing the protein sequences of the two paralogs. An alignment of SEC10a and SEC10b protein sequences showed substitutions of four amino acid residues and an indel four amino acid residues long (Figure S4). Three of the substitutions are more or less synonymous with respect to their biochemical and sterical properties and we suppose no major difference in the structure of the two SEC10 proteins. The fourth substitution, T629P, was considered potentially more consequential because a proline substitution could conceivably disrupt an α-helical structure, which is dominant and functionally essential in all exocyst subunits [41–43]. However, no α-helix is predicted (using Jalview 2.8; http://www.jalview.org/) in this region or in the indel region of SEC10.

In yeast and metazoans, major phenotypic defects resulting from affected vesicle trafficking have been found for overexpression of dominant-negative variants, deletion or knockdown of the Sec10 exocyst subunit [44–46]. It is likely that the SEC10 exocyst subunit is essential in Arabidopsis and total loss of the SEC10 function would cause a severe phenotypic deviation in Arabidopsis as well, similarly to loss-of-function exocyst mutants in SEC6 and SEC8 (both encoded by single genes) and a double mutant in SEC5a SEC5b that all exhibit a complete pollen-germination defect due to impaired pollen tube germination and growth [29,31]. Since generation of sec10a sec10b double mutants in Arabidopsis by crossing is impractical due to extremely tight genetic linkage, further experiments, including a knockdown of both SEC10 genes are required to test this hypothesis. A strategy employing inducible RNAi expression would have to be used in plants with careful characterization of the efficiency of an inhibitory construct, bearing also in mind the expected essential role of the SEC10 exocyst subunit. So far, the lack of observable phenotypic deviations in mutants for either copy of sec10, together with minimal differences in protein sequences of SEC10a and SEC10b, point to functional redundancy of these duplicated genes. It would be interesting to reinvestigate the actual number of gene copies in other cases of knock-outs of “single-copy” genes with a surprising lack of a mutant phenotype.

When did the SEC10 duplication occur in evolution? We found that the duplication is present in at least three different ecotypes of A. thaliana, but we could not experimentally detect any SEC10 tandem duplication in A. lyrata. In addition, A. thaliana SEC10a and SEC10b are mutually more similar than any of them to the A. lyrata SEC10 (Data S2). This indicates that the duplication most likely occurred after the divergence of the two Arabidopsis species. Experimental examination of additional Arabidopsis species and other genera of the Brassicaceae family is, however, necessary to make such a statement robust. Nevertheless, the apparently recent origin of the SEC10 duplication may suggest that it might not yet passed the fixation stage [2], and that it perhaps may not be stable in the long term. Indeed, genes encoding interaction-rich proteins, such as subunits of highly interconnected protein complexes, tend to tolerate tandem duplications rather poorly [7].

Although the observed duplication of a functional gene conflicts with the balance hypothesis, which proposes that single-gene duplication of genes coding for the subunits of protein complexes should be deleterious [47], it is compatible with the hypothesis that duplicated genes provide genetic robustness against null mutations [48], as well as with the possibility that subtle subfunctionalization of duplicated genes may contribute to robustness towards
“epigenetic load” [49], especially in sessile organisms. Single knockout data from 5360 A. thaliana lines indicate that duplicated genes play a significant role in functional compensation, where duplications tend to persist for a longer time in case of a more severe phenotype of single knock-outs than in the case of a less severe phenotype [50].

Conclusions

To summarize, we report here a hitherto undocumented A. thaliana gene duplication that has resulted in the omission of a functional, expressed gene from the reference genome sequence, due to a sequence assembly error. Similarly to mammalian genomes, some nearly identical gene duplications remain hidden in the current reference sequence of a presumably well-characterized genome of Arabidopsis thaliana (and possibly other genomes), and such errors may even propagate in sequencing of new Arabidopsis accessions or related species. Since the evidence presented in this paper does not currently meet all the criteria for A. thaliana reference sequence update, as stated in the corresponding TAIR policy and as employed in the genome maintenance and (re)annotation process [http://Arabidopsis.org/doc/portals/genAnnotation/gene_structural_annotation/ref_genome_sequence/11413 and [8]], we would like to encourage researchers responsible for the A. thaliana genome sequencing to perform an independent re-sequencing of the SEC10 locus and update the reference genome sequence of A. thaliana. In addition, if original sequence reads are still available, re-assemblying of the whole genome sequence from original sequence reads using up-to-date approaches would be advisable to reveal possible similar instances of missed genes.

Materials and Methods

Plants, cultivation and genotyping

A. thaliana Columbia-0 (Col-0) plants were used for all experiments unless stated otherwise, Landsberg erecta (Ler-0) and Nossen (No-0) ecotypes, together with Arabidopsis lyrata (Magnus Noodborg, GMI, Vienna), were also included for an analysis of the SEC10 gene duplication.

T-DNA insertion mutant lines are listed in Table S1, Table 1 and Figure 4. Seeds were obtained from either NASC [51] or GABI-Kat [52]. Each T-DNA line was backcrossed to Col-0.

To analyze the expression level of SEC10a and SEC10b, total cDNA was prepared from 100 mg of Col-0 7-day-old seedlings using the RNeasy Plant Mini Kit (Qiagen) followed by RT-PCR using the Transcriptor High Fidelity cDNA Synthesis Kit (Roche) according to manufacturers instructions. The coding sequence of the SEC10a cDNA was cloned analogically, but from total cDNA prepared from homozygous sec10b mutants (SALK_120710). Cloning primers, S10-Start and S10-Stop (Table S3), matching both SEC10 copies and starting at the start and stop codons, respectively, were used. PCR products were cloned into the pJET1.2/blunt cloning vector (Fermentas). For cloning of SEC10b, the coding sequence of SEC10b cDNA was cloned analogically from total cDNA prepared from homozygous sec10b mutants (SALK_120710). Cloning primers, S10-Start and S10-Stop (Table S3), matching both SEC10 copies and starting at the start and stop codons, respectively, were used. PCR products were cloned into the pJET1.2/blunt cloning vector (Fermentas). For analysis of the SEC10 identity, the coding sequence of SEC10 was amplified from each clone tested and digested by the BpiI restriction enzyme (Fermentas) that allows to discriminate between SEC10a and SEC10b (Figure S4B). BpiI cuts SEC10b (2490 bp total length) at four positions (78, 392, 681 and 1867 bp), while SEC10a (2478 bp) at three positions only (78, 392 and 681 bp).

Expression analysis in tissues and mutant plants

To analyze the expression level of SEC10a and SEC10b, total cDNA was prepared from 100 mg of young seedlings (7-day-old), roots (14-day-old), true leaves and flowers (both from one-month-old plants) using the RNeasy Plant Mini Kit (Qiagen) followed by the RT-PCR Transcriptor High Fidelity cDNA Synthesis Kit (Roche). RNA concentration was measured using NanoDrop 1000 (Thermo Scientific). Plasmid clones pda16746 and pda07158 carried SEC10a and SEC10b cDNA. Plasmid clones pda16746 and pda07158 carrying AK222187 and AY096638 (NCBI) were sequenced using the CloneJET PCR Cloning Kit (Fermentas) following the Blunt-End Cloning protocol.

Cloning of SEC10a and SEC10b cDNA

The clone APZL19f10R, represented by the EST sequence GenBank:AV528809, was identified by BLAST [http://blast.ncbi.nlm.nih.gov/] as the SEC10 cDNA clone with the longest 5’ UTRs preceding the predicted coding sequence, and was therefore selected for complete sequencing. The clone was obtained from the Kazusa DNA Research Institute [http://est.kazusa.or.jp/ea/ plant/arabidopsis/EST/], subcloned, and sequenced. The assembled sequence was trimmed for vector sequences and deposited in GenBank with the accession number AF479280. The gene corresponding to this cDNA is now called SEC10a.

The coding sequence of the SEC10b cDNA was also amplified and cloned from total cDNA prepared from 100 mg of Col-0 7-day-old seedlings using the RNeasy Plant Mini Kit (Qiagen) followed by RT-PCR using the Transcriptor High Fidelity cDNA Synthesis Kit (Roche) according to manufacturers instructions. The coding sequence of the SEC10a cDNA was cloned analogically, but from total cDNA prepared from homozygous sec10b mutants (SALK_120710). Cloning primers, S10-Start and S10-Stop (Table S3), matching both SEC10 copies and starting at the start and stop codons, respectively, were used. PCR products were cloned into the pJET1.2/blunt cloning vector (Fermentas). For analysis of the SEC10 identity, the coding sequence of SEC10 was amplified from each clone tested and digested by the BpiI restriction enzyme (Fermentas) that allows to discriminate between SEC10a and SEC10b (Figure S4B). BpiI cuts SEC10b (2490 bp total length) at four positions (78, 392, 681 and 1867 bp), while SEC10a (2478 bp) at three positions only (78, 392 and 681 bp).
specific amplification of each SEC10 copy. Semi-quantitative PCR was performed using the DreamTaq polymerase (Thermo Scientific) and S10-Start primer matching both SEC10 copies and S10a-3UTR or S10b-3UTR primers matching specifically SEC10a or SEC10b, respectively (Table S3). Actin-specific primers (ACT7-fw and ACT7-rv; Table S3) were used as a control of the template concentration. Annealing temperatures used in PCR reactions were 59°C for SEC10a, 62°C for SEC10b, and 62°C for ACT7. Number of PCR cycles was 32 for SEC10 genes, 34 for controls and 25 for ACT7.

**Supporting Information**

**Figure S1** Tandem duplication of the SEC10 gene in other Arabidopsis accessions.

**Figure S2** Dot plot of the SEC10 locus.

**Figure S3** Alignment of predicted SEC10a and SEC10b protein sequences.

**Figure S4** Analysis of SEC10 expression in A. thaliana.

**Table S1** Segregation ratio of sec10 mutant lines.

**Table S2** Assignment of previously published SEC10 cDNA sequences to the two SEC10 paralogs.

**Table S3** List of primers used in this study.

**Data S1** Alignment of SEC10a and SEC10b genes including their flanking sequences. Sequences of SEC10a and SEC10b genes from the revisited SEC10 locus [EMBL: HG764169] were aligned using Clustal X2.1 [57]. Exon-intron borders were manually corrected. The file can be opened in Clustal W, BioEdit, Jalview or similar software. (ALN)

**Data S2** Alignment of A. thaliana SEC10a and SEC10b genes with the A. lyrata SEC10 gene. Sequences of A. thaliana SEC10a and SEC10b genes from the revised SEC10 locus [EMBL: HG764169] and the sole A. lyrata SEC10 gene (GenBank: ADDBK01001175.1, nucleotides 173660–167031, complementary strand) were aligned using Clustal X2.1 [57]. The file can be opened in Clustal W, BioEdit, Jalview or similar software. (ALN)

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**Author Contributions**

Conceived and designed the experiments: LS FC RC VZ JEF. Performed the experiments: NV RC LS. Analyzed the data: LS FC ME RC. Wrote the paper: LS ME FC NV.

**References**