



## Widespread anti-sense transcription in apple is correlated with siRNA production and indicates a large potential for transcriptional and/or post-transcriptional control

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Auteur	Celton, Jean-Marc [1], Gaillard, Sylvain [2], Bruneau, Maryline [3], Pelletier, Sandra [4], Aubourg, Sébastien [5], Martin-Magniette, Marie-Laure [6], Navarro, Lionel [7], Laurens, François [8], Renou, Jean-Pierre [9]
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Résumé en anglais	<p>Characterizing the transcriptome of eukaryotic organisms is essential for studying gene regulation and its impact on phenotype. The realization that anti-sense (AS) and noncoding RNA transcription is pervasive in many genomes has emphasized our limited understanding of gene transcription and post-transcriptional regulation. Numerous mechanisms including convergent transcription, anti-correlated expression of sense and AS transcripts, and RNAi remain ill-defined. Here, we have combined microarray analysis and high-throughput sequencing of small RNAs (sRNAs) to unravel the complexity of transcriptional and potential post-transcriptional regulation in eight organs of apple (<i>Malus × domestica</i>). The percentage of AS transcript expression is higher than that identified in annual plants such as rice and <i>Arabidopsis thaliana</i>. Furthermore, we show that a majority of AS transcripts are transcribed beyond 3'UTR regions, and may cover a significant portion of the predicted sense transcripts. Finally we demonstrate at a genome-wide scale that anti-sense transcript expression is correlated with the presence of both short (21-23 nt) and long (&gt; 30 nt) siRNAs, and that the sRNA coverage depth varies with the level of AS transcript expression. Our study provides a new insight on the functional role of anti-sense transcripts at the genome-wide level, and a new basis for the understanding of sRNA biogenesis in plants.</p>
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