

## SUPPLEMENTAL MATERIALS

### An updated perspective on *Sinorhizobium meliloti* chemotaxis to alfalfa flavonoids

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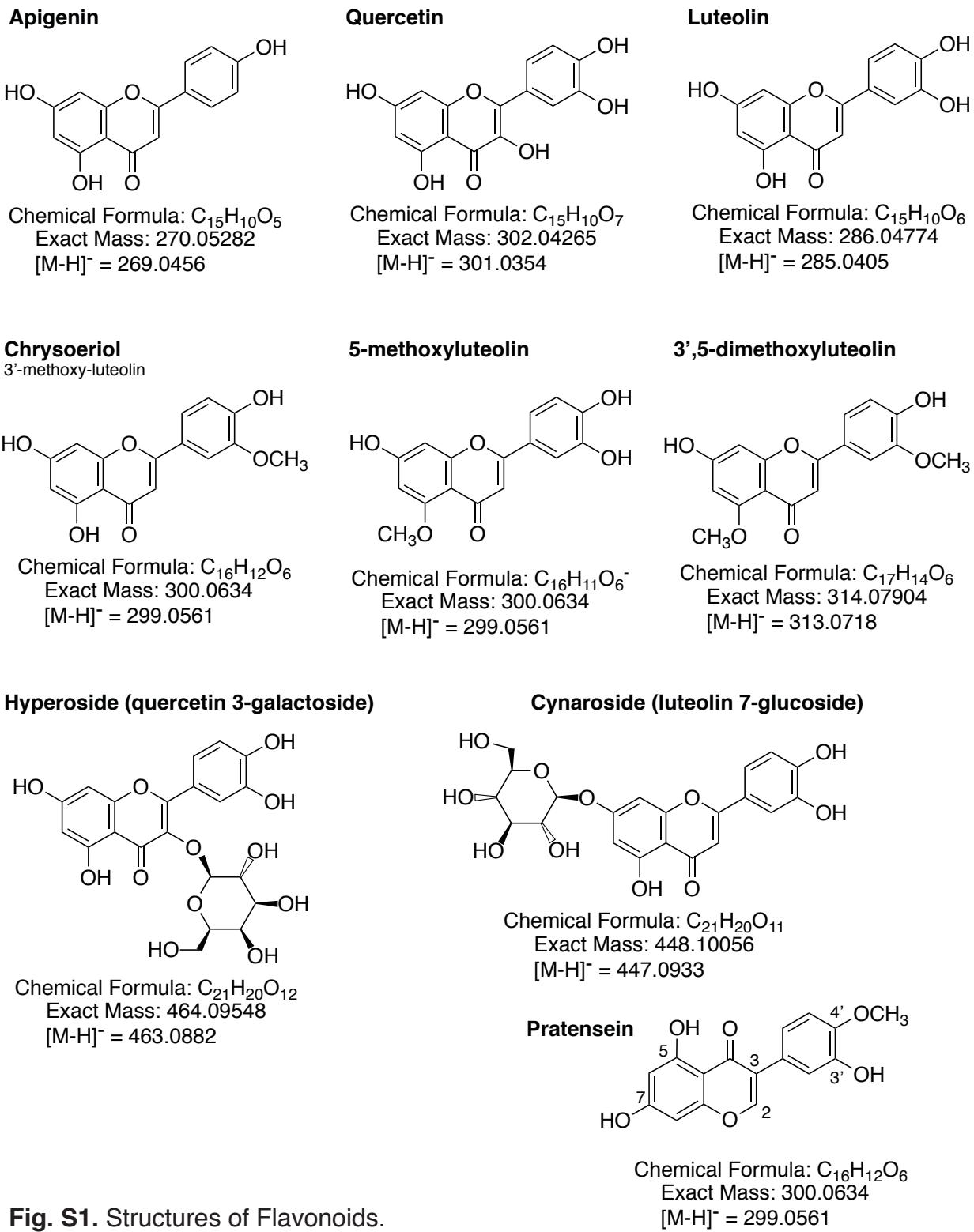
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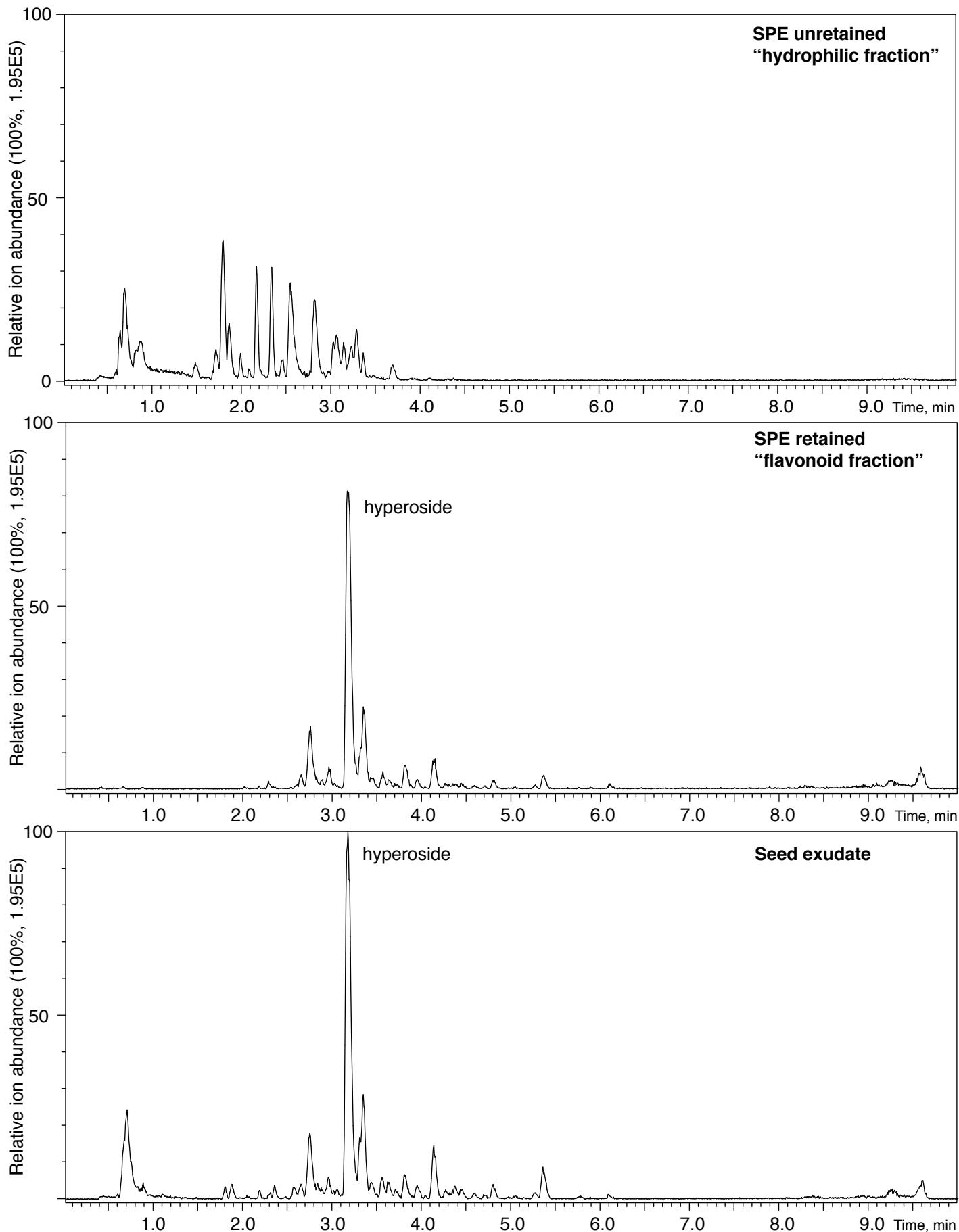
**Fig. S2.** LC-MS Chromatograms in Base Peak Mode. Traces are normalized to relative ion abundance of hyperoside in the original seed exudate. “Fast gradient” LC conditions.

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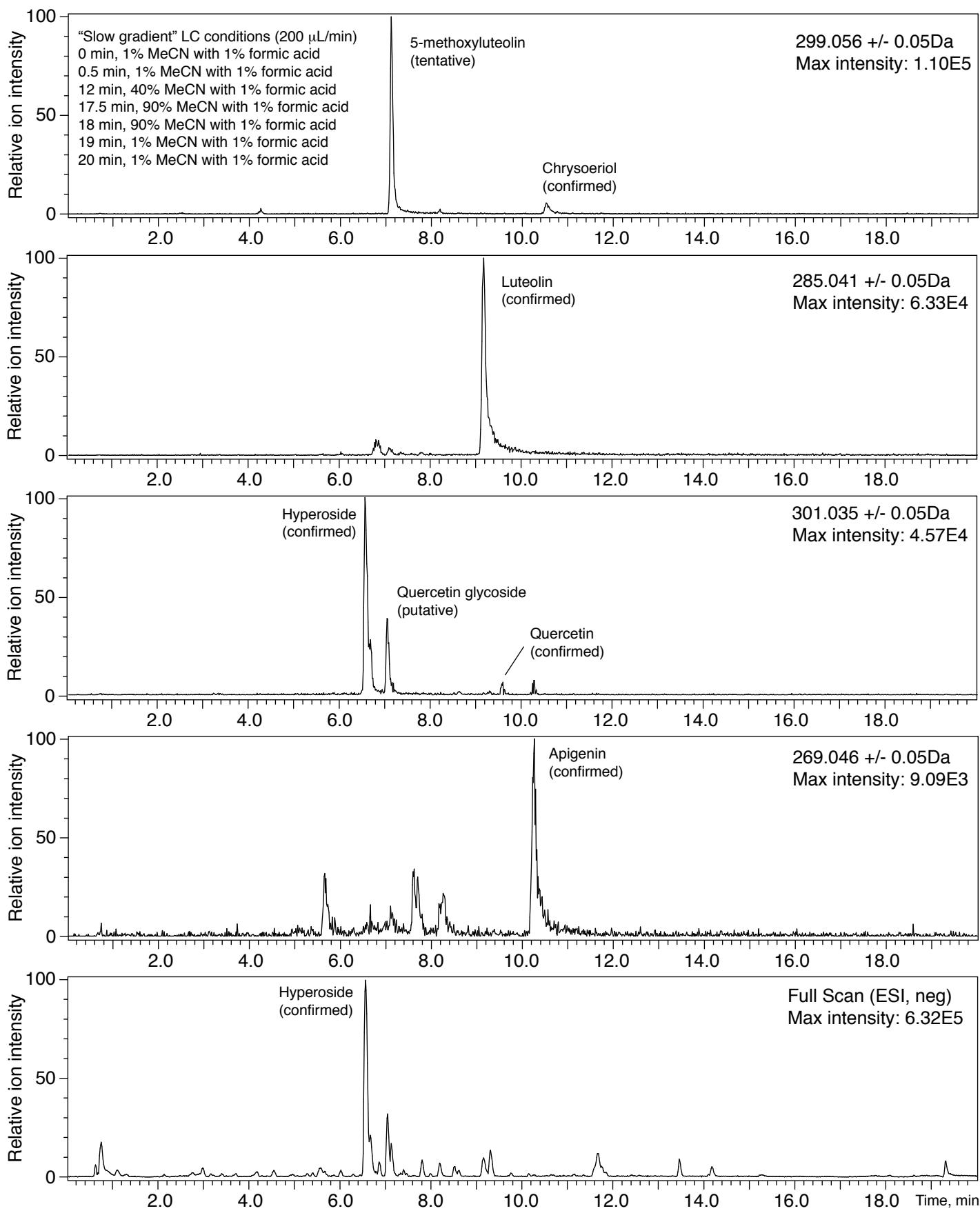
**Fig. S4.** Selected Ion Monitoring for Luteolin- and Quercetin-based Compounds.



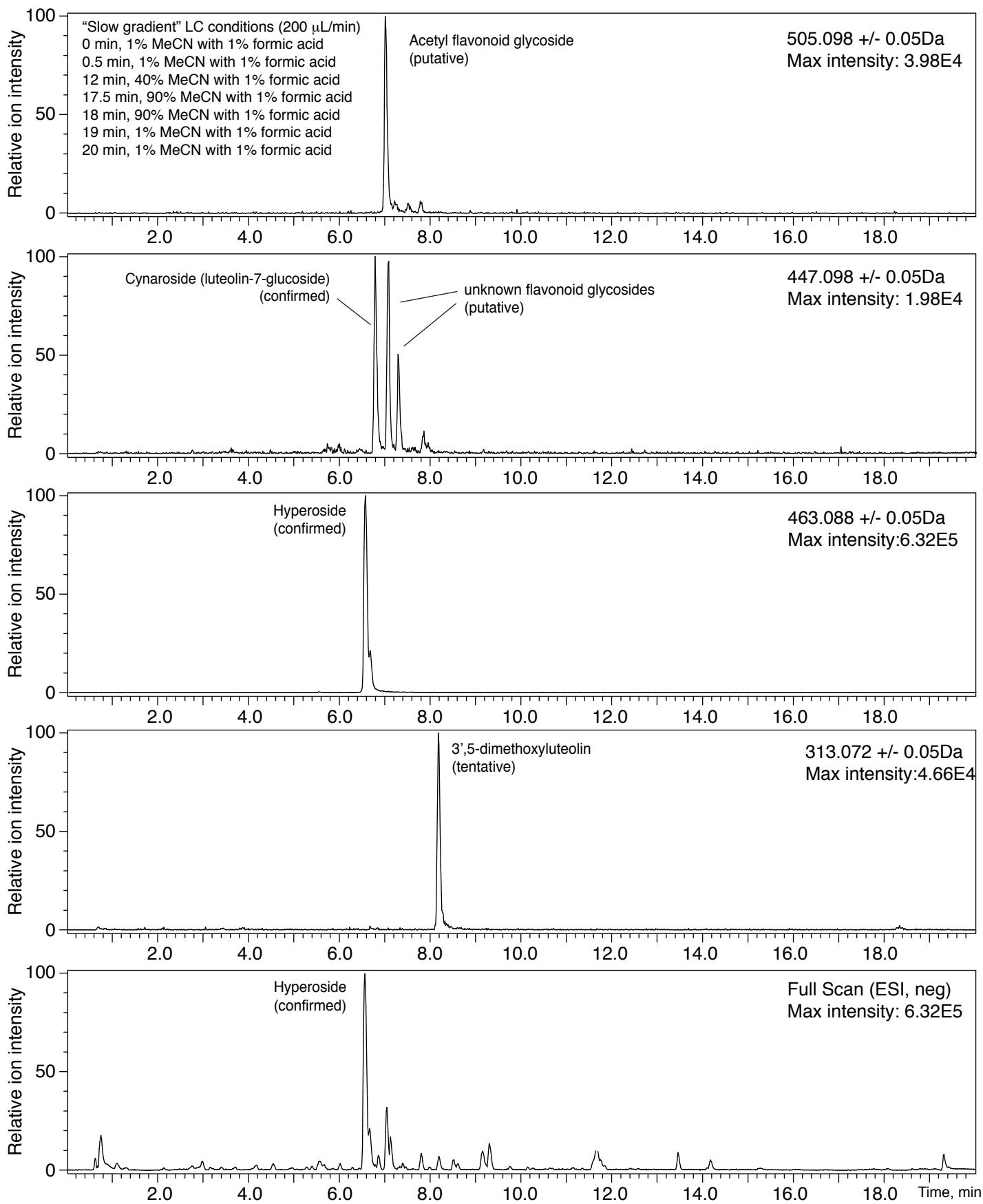
**Fig. S1.** Structures of Flavonoids.



**Fig. S2.** LC-MS Chromatogram in Base Peak Mode. Traces are normalized to relative ion abundance of hyperoside in the original seed exudate. “Fast gradient” LC conditions. Hyperoside was confirmed with an authentic standard (retention time, parent mass, and fragmentation pattern).



**Fig. S3.** Selected Ion Monitoring for Luteolin-, Quercetin- and Apigenin-based Compounds. Confirmed: authentic standard, retention time, parent mass, and fragmentation pattern matches. Tentative: previous literature, no authentic standard. Putative: parent mass and fragmentation pattern only.



**Fig. S4.** Selected Ion Monitoring for Luteolin- and Quercetin-based Compounds. Confirmed: authentic standard, retention time, parent mass, and fragmentation pattern matches. Tentative: previous literature, no authentic standard. Putative: parent mass and fragmentation pattern only.