**New Phytologist Supporting Information, Evidence for host-microbiome co-evolution in apple. Ahmed Abdelfattah, Ayco J.M. Tack, Birgit Wasserman, Jia Liu, Gabriele Berg, John Norelli, Samir Droby, Michael Wisniewski. 18 October 2021.**

**Table S2.** The supplementary document includes the accession and sequences of Malus species, the calculated distances, and the phylogenetic trees.

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>EF113171.1 Malus kansuensis
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[1] #EF113171.1_M. kansuensis [2] #JQ392462.1_M. sylvestris [3] #MH270485.1_M. yunnanensis [4] #JQ392445.1_M. prattii [5] #JQ392448.1_M. ioensis [6] #AF186525.1_M. coronaria [7] #AF186523.1_M. angustifolia [8]#MK386850.1_M. orientalis [9] #AF186492.1_M. sieversii [10]#AF186478.1_M. domestica [11] #JQ392463.1_M. prunifolia

| [1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 ] |
|---|---|---|---|---|---|---|---|---|---|---|
| [ 1] | | | | | | | | | | |
| [ 2] | 0.0732 | | | | | | | | | |
| [ 3] | 0.0258 | 0.075 | | | | | | | | |
| [ 4] | 0.0259 | 0.0714 | 0.0051 | | | | | | | |
| [ 5] | 0.0529 | 0.0692 | 0.0584 | 0.0548 | | | | | | |
| [ 6] | 0.0475 | 0.0673 | 0.0529 | 0.0493 | 0.0051 | | | | | |
| [ 7] | 0.0475 | 0.0637 | 0.0529 | 0.0494 | 0.0034 | 0.0017 | | | | |
| [ 8] | 0.0549 | 0.0383 | 0.0567 | 0.0531 | 0.0456 | 0.0437 | 0.0402 | | | |
| [ 9] | 0.0549 | 0.0384 | 0.0567 | 0.0531 | 0.0492 | 0.0474 | 0.0438 | 0.0034 | | |
| [10] | 0.0549 | 0.0384 | 0.0567 | 0.0531 | 0.0492 | 0.0474 | 0.0438 | 0.0085 | 0.0051 | |
| [11] | 0.0458 | 0.0295 | 0.0475 | 0.044 | 0.0402 | 0.0384 | 0.0349 | 0.0085 | 0.0085 | 0.0068 |

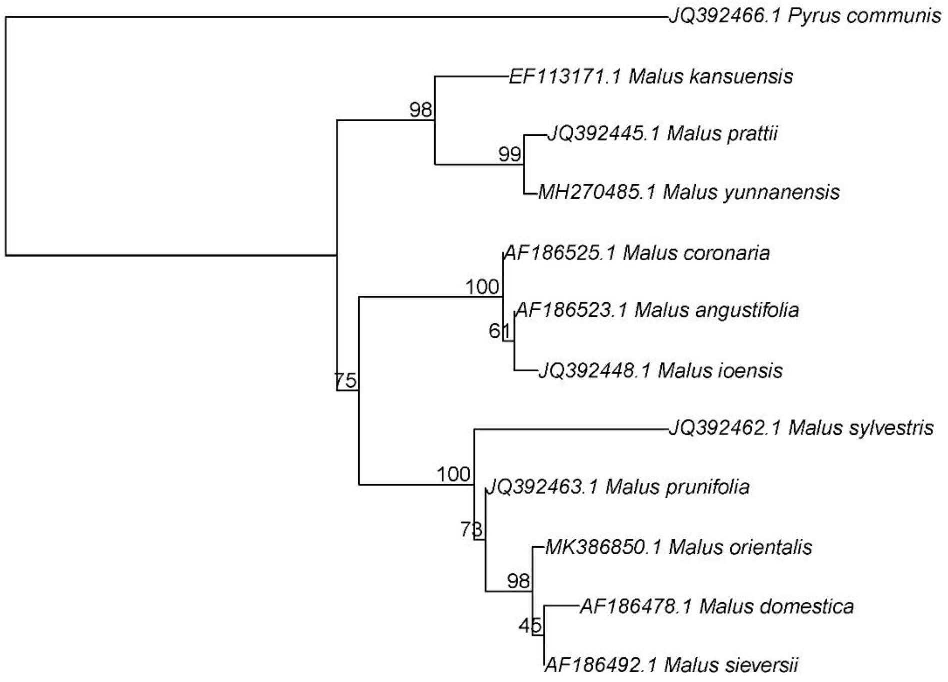

**Table S3** Analysis of Variance on the effect of domestication and Malus phylogeny (species) on fungal and bacterial diversity based on Shannon index. In "Domestication" compares the three Domestication groups i.e. M. domestica, apple progenitor species (M. sieversii, M. orientalis, M. prunifolia, and M. sylvestris), and non-progenitor Malus species (M. kansuensis, M. yunnanensis, M. angustifolia, M. coronaria, M. ioensis, M. prattii). Degrees of freedom for domestication was 2 and for species 8.

| | Fungi | | | | Bacteria | | | |
|---|---|---|---|---|---|---|---|---|
| | Domestication | | Species | | Domestication | | Species | |
| | *F* | *P* | *F* | *P* | *F* | *P* | *F* | *P* |
| Richness | 9.143 | 0.0048 | 1.513 | 0.178 | 0.143 | 0.867 | 0.856 | 0.559 |
| Evenness | 1.470 | 0.2399 | 2.132 | 0.048 | 2.213 | 0.120 | 1.833 | 0.093 |
| Diversity (Shannon) | 5.004 | 0.0012 | 1.394 | 0.071 | 0.686 | 0.508 | 0.906 | 0.519 |

**Table S4** Results of statistical pairwise-comparisons of fungal and bacterial diversity based on Shannon index and community composition based on Bray-Curtis dissimilarity index using adonis (~Permanova). P values were adjusted using FDR method for both tests. The test was done to compare the three Domestication groups i.e. M. domestica, apple progenitor species (M. sieversii, M. orientalis, M. prunifolia, and M. sylvestris), and wild Malus species (M. kansuensis, M. yunnanensis, M. angustifolia, M. coronaria, M. ioensis, M. prattii).

| | | Permanova | | Shannon | Richness | Evenness |
|---|---|---|---|---|---|---|
| | | $R^2$ | *P* | *P* | *P* | *P* |
| Fungi | Wild vs Progenitors | 0.033 | 0.038 | 0.003 | 0.004 | 0.272 |
| | Wild vs Domesticated | 0.053 | 0.006 | 0.006 | 0.001 | 0.566 |
| | Progenitors vs Domesticated | 0.033 | 0.038 | 0.983 | 0.757 | 0.911 |
| Bacteria | Wild vs Progenitors | 0.047 | 0.003 | 0.459 | 0.890 | 0.561 |
| | Wild vs Domesticated | 0.062 | 0.003 | 0.528 | 0.980 | 0.160 |
| | Progenitors vs Domesticated | 0.029 | 0.123 | 0.998 | 0.966 | 0.594 |