# APPENDIX A. Supporting tables on NE9 crop importance and the PGRU conservation and distribution activities, US Production Data from National Agricultural Statistics Service (2017).

Table 1. Importance of the PGRU's vegetables and fruits to the U.S.

|  |  |
| --- | --- |
| **Crops** | **Value paid to grower in****millions of dollars, 2017** |
| Artichokes | 65.5 |
| Asparagus | 73.1 |
| Broccoli | 926.1 |
| Cabbage | 428.7 |
| Cauliflower | 387.0 |
| Celery | 314.7 |
| Onions | 971.2 |
| Squash | 178.5 |
| Tomatoes | 1674.1 |
| **Total vegetables** | **5018.9** |
| Grapes | 6257.2 |
| Apples | 3462.5 |
| Tart Cherries | 89.4 |
| **Total fruits** | **9809.1** |

Table 2. Importance of PGRU vegetables and fruits worldwide (FAOSTAT, 2017).

|  |  |
| --- | --- |
| **Crops** | **Production in million** **metric tons, 2016** |
| Artichokes | 1.5 |
| Asparagus | 8.7 |
| Brassicas | 71.3 |
| Buckwheat | 2.4 |
| Onions | 98.9 |
| Squash | 26.5 |
| Tomatoes | 177.0 |
| **Total vegetables** | **384.8** |
| Grapes | 77.4 |
| Apples | 89.3 |
| Tart Cherries | 1.4 |
| **Total fruits** | **168.1** |

Table 3. Number of **samples** distributed from PGRU **seed** collections from 2013-2017 by cooperator type.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Cooperator Type** | **2013** | **2014** | **2015** | **2016** | **2017** | **Total** |
| Foreign, Commercial Companies | 221 | 1406 | 2551 | 2143 | 952 | 7273 |
| Foreign genebank/genetic resource units | 322 | 0 | 435 | 105 | 231 | 1093 |
| Foreign Individuals | 0 | 47 | 34 | 0 | 9 | 90 |
| CGIAR International Agriculture Research Centers | 0 | 0 | 0 | 0 | 0 | 0 |
| Foreign Public Organizations (gov) | 1599 | 617 | 945 | 1937 | 1174 | 6272 |
| US State Agencies & All Universities | 583 | 1404 | 1466 | 931 | 1124 | 5508 |
| US Agency for International Development | 0 | 0 | 0 | 3 | 102 | 105 |
| USDA, ARS | 202 | 53 | 301 | 549 | 68 | 1173 |
| USA Commercial Companies | 513 | 1107 | 642 | 272 | 1976 | 4510 |
| Other USA Federal Agencies | 11 | 5 | 0 | 0 | 276 | 292 |
| USA Individuals | 325 | 246 | 201 | 163 | 144 | 1079 |
| US Non-profit Organizations | 217 | 194 | 312 | 777 | 197 | 1697 |
| **Total** | **3993** | **5079** | **6887** | **6880** | **6253** | **33466** |

Table 4. Number of **accessions** distributed from PGRU **seed** collections from 2013-2017 by cooperator type.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Cooperator Type** | **2013** | **2014** | **2015** | **2016** | **2017** | **Total** |
| Foreign, Commercial Companies | 221 | 1406 | 2551 | 2143 | 952 | 7273 |
| Foreign genebank/genetic resource units | 322 | 0 | 435 | 105 | 231 | 1093 |
| Foreign Individuals | 0 | 47 | 34 | 0 | 9 | 90 |
| CGIAR International Agriculture Research Centers | 0 | 0 | 0 | 0 | 0 | 0 |
| Foreign Public Organizations (gov) | 1599 | 617 | 945 | 1937 | 1174 | 6272 |
| US State Agencies & All Universities | 583 | 1404 | 1466 | 931 | 1124 | 5508 |
| US Agency for International Development | 0 | 0 | 0 | 3 | 102 | 105 |
| USDA, ARS | 202 | 53 | 301 | 549 | 68 | 1173 |
| USA Commercial Companies | 513 | 1107 | 642 | 272 | 1976 | 4510 |
| Other USA Federal Agencies | 11 | 5 | 0 | 0 | 276 | 292 |
| USA Individuals | 325 | 246 | 201 | 163 | 144 | 1079 |
| US Non-profit Organizations | 217 | 194 | 312 | 777 | 197 | 1697 |
| **Total** | **3993** | **5079** | **6887** | **6880** | **6253** | **29092** |

Table 5. Number of **samples** distributed from PGRU **clonal** collections from 2013-2017 by cooperator type.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Cooperator Type** | **2013** | **2014** | **2015** | **2016** | **2017** | **Total** |
| Foreign, Commercial Companies | 11 | 4 | 0 | 0 | 8 | 23 |
| Foreign genebank/genetic resource units | 0 | 0 | 4 | 16 | 4 | 24 |
| Foreign Individuals | 88 | 90 | 59 | 38 | 106 | 381 |
| CGIAR International Agriculture Research Centers | 0 | 0 | 0 | 0 | 0 | 0 |
| Foreign Public Organizations (gov) | 151 | 99 | 202 | 45 | 16 | 513 |
| US State Agencies & All Universities | 1139 | 637 | 1102 | 428 | 1575 | 4881 |
| US Agency for International Development | 0 | 0 | 0 | 0 | 0 | 0 |
| USDA, ARS | 2055 | 2005 | 1355 | 1079 | 817 | 7311 |
| USA Commercial Companies | 481 | 591 | 689 | 583 | 514 | 2858 |
| Other USA Federal Agencies | 0 | 18 | 0 | 0 | 10 | 28 |
| USA Individuals | 1579 | 2565 | 3150 | 3511 | 3493 | 14298 |
| US Non-profit Organizations | 247 | 262 | 206 | 276 | 294 | 1285 |
| **Total** | **5751** | **6271** | **6767** | **5976** | **6837** | **31602** |

Table 6. Number of **accessions** distributed from PGRU **clonal** collections from 2013-2017 by cooperator type.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Cooperator Type** | **2013** | **2014** | **2015** | **2016** | **2017** | **Total** |
| Foreign, Commercial Companies | 10 | 4 | 0 | 0 | 8 | 22 |
| Foreign genebank/genetic resource units | 0 | 0 | 4 | 16 | 4 | 24 |
| Foreign Individuals | 35 | 42 | 33 | 23 | 56 | 189 |
| CGIAR International Agriculture Research Centers | 0 | 0 | 0 | 0 | 0 | 0 |
| Foreign Public Organizations (gov) | 142 | 95 | 198 | 45 | 16 | 496 |
| US State Agencies & All Universities | 682 | 525 | 591 | 344 | 984 | 3126 |
| US Agency for International Development | 0 | 0 | 0 | 0 | 0 | 0 |
| USDA, ARS | 450 | 418 | 645 | 459 | 352 | 2324 |
| USA Commercial Companies | 379 | 432 | 481 | 433 | 386 | 2111 |
| Other USA Federal Agencies | 0 | 18 | 0 | 0 | 10 | 28 |
| USA Individuals | 892 | 1236 | 1302 | 1428 | 1468 | 6326 |
| US Non-profit Organizations | 215 | 229 | 180 | 231 | 247 | 1102 |
| **Total** | **2805** | **2999** | **3434** | **2979** | **3531** | **15748** |

Table 7. Number of samples and accessions distributed to NE9 states from 2013-2017.

|  |  |  |
| --- | --- | --- |
| **State** | **Clonal**  | **Seeds** |
| **Samples**  | **Accessions** | **Samples** | **Accessions** |
| Connecticut | 77 | 60 | 66 | 66 |
| Delaware | 0 | 0 | 0 | 0 |
| Maine | 411 | 290 | 32 | 32 |
| Maryland | 248 | 192 | 51 | 51 |
| Massachusetts | 284 | 223 | 97 | 97 |
| New Hampshire | 197 | 167 | 28 | 28 |
| New Jersey | 46 | 43 | 235 | 223 |
| New York | 9876 | 2347 | 2322 | 2250 |
| Pennsylvania | 659 | 443 | 160 | 155 |
| Rhode Island | 5 | 5 | 1 | 1 |
| Vermont | 166 | 158 | 18 | 18 |
| West Virginia | 921 | 468 | 76 | 76 |
| **Total** | **12890** | **4396** | **3086** | **2997** |

**Appendix B:** Recent Select PGRU References from 2013 to 2017

**2013**

Gross, B.L., G.M. Volk, C.M. Richards, P.A. Reeves, A.D. Henk, P.L. Forsline, A. Szewc-McFadden, G. Fazio, and C.T. Chao. 2013. Diversity captured in the USDA-ARS National Plant Germplasm System apple core collection. J. Amer. Soc. Hort. Sci. 138(5):375-381.

Miller, A.J., N. Matasci, H. Schwaninger, M.K. Aradhya, B. Prins, G.-Y. Zhong, C. Simon, E.S. Buckler, and S. Myles. 2013. *Vitis* phylogenomics: hybridization intensities from a SNP array outperform genotype calls. PlosOne:e78680.

Panthee, D.R., J.A. Labate and L.D. Robertson. 2013. Evaluation of tomato accessions for flavour and flavour-contributing components. Plant Genetic Resources: Characterization & Utilization 11:106-113.

Panthee, D.R., J.A. Labate, L.D. Robertson, M.T. McGrath and A.P. Breksa III. 2013. Genotype x environmental interaction for fruit quality traits in vintage tomato varieties. Euphytica 193:169-182*.*

Sawler, J., B. Reisch, M.K. Aradhya, B. Prins, G.-Y. Zhong, H. Schwaninger, C. Simon, E. Buckler, and S. Myles. 2013. Genomics assisted ancestry deconvolution in grape. PlosOne 8(11): e80791.

Volk G.M., A.D. Henk, C.M. Richards, P.L. Forsline, and C.T. Chao. 2013. *Malus sieversii*: a diverse Central Asian apple species. HortScience 48(12):1440-1444.

Wan, Y., H.R. Schwaninger, A.M. Baldo, J.A. Labate, G.-Y. Zhong and C.J. Simon. 2013. A phylogenetic analysis of the grape genus (*Vitis* L.) reveals broad reticulation and concurrent diversification during Neogene and Quaternary climate change. BMC Evol. Biol. 13:141.

**2014**

Fazio, G., C.T. Chao, P.L. Forsline, C. Richards, and G. Volk. 2014. Tree and root architecture of *Malus sieversii* seedlings for rootstock breeding. Proc. Xth IS on Integrating Canopy, Rootstock and Environmental Physiology in Orchard Systems. Acta Hort. 1058:585-594.

Labate, J.A., L.D. Robertson, S.R. Strickler, and L.A. Mueller. 2014. Genetic structure of the four wild tomato species in the *Solanum peruvianum* s.l. species complex. Genome 57:169-180.

Li, H.K., Y.Z. Wan, and C.J. Simon. 2014. Characterisation of patterns of genetic differentiation within and among Euvitis species based on a large number of nuclear single‐nucleotide polymorphisms. Aus. J. Grape & Wine Res. 20(3):507-518.

Liang, [Z.](http://www.pubfacts.com/author/Zhenchang%2BLiang), [L. Cheng](http://www.pubfacts.com/author/Lailiang%2BCheng), [G.-Y. Zhong](http://www.pubfacts.com/author/Gan-Yuan%2BZhong), and [R.H. Liu](http://www.pubfacts.com/author/Rui%2BHai%2BLiu). 2014. [Antioxidant and antiproliferative activities of twenty-four *Vitis vinifera* grapes](http://www.pubfacts.com/detail/25133401/Antioxidant-and-antiproliferative-activities-of-twenty-four-Vitis-vinifera-grapes). PLosOne 9(8):e105146.

Perazzolli, M., G. Malacarne, A.M. Baldo, L. Righetti, A. Bailey, P. Fontana, R. Velasco, and M. Malnoy. 2014. Characterization of resistance gene analogues (RGAs) in apple (*Malus x domestica* Borkh.) and their evolutionary history of the Rosaceae family. PLosOne. 9(2):e83844.

Yang, Y., J. Labate, Z. Liang, P. Cousins, B. Prins, J. Preece, M. Aradhya, and G.-Y. Zhong. 2014. Multiple loss-of-function *5-O-Glucosyltransferase* alleles revealed in *Vitis vinifera*, but not in other *Vitis* species**.**  Theor. Appl. Genet. 127(11):2433-2451.

**2015**

Bai, Y., L. Dougherty, L. Cheng, G.-Y. Zhong, and K. Xu. 2015. Uncovering co-expression gene network modules regulating fruit acidity in diverse apples. BMC Genomics 16(1):612.

Breksa III, A.P., L.D. Robertson, J.A. Labate, B.A. King, and D.E. King. 2015. Physicochemical and morphological variation in tomato fruit: implications for improved quality, size and shape components. J. Food Comp. Anal. 42:16-25.

Labate, J.A. and L.D. Robertson. 2015. Nucleotide diversity estimates of tomatillo (*Physalis philadelphica*) accessions including nine new inbred lines. Mol. Breeding 35:106.

Money D., K.M. Gardner, Z. Migicovsky, H. Schwaninger, G.Y. Zhong, and S. Myles. 2015. LinkImpute – fast and accurate genotype imputation for non-model organisms. G3: Genes, Genomes, Genetics 5:2383.

Sugimoto N., P. Forsline, and R. Beaudry. 2015. Volatile profiles of members of the USDA Geneva *Malus* Core collection: utility in evaluation of a hypothesized biosynthetic pathway for esters derived from 2‑Methylbutanoate and 2‑Methylbutan-1-ol. J. Ag. Food Chem. 63:2016-2116.

VolkG.M., C.T. Chao, J. Norelli, S.K. Brown, G. Fazio, C. Peace, J. McFerson, G.-Y. Zhong, and P. Bretting. 2015. The vulnerability of U.S. apple genetic resources. Genet. Res. & Crop Evol. 62:765-794. DOI 10.1007/s10722-014-0194-2.

Volk, G.M., A.D. Henk, A. Baldo, G. Fazio, C.T. Chao, and C.M. Richards. 2015. Chloroplast heterogeneity and historical admixture within the genus *Malus*. Amer. J. Botany 102(7):1-11.

**2016**

Janisiewicz, W.J.,B. Nichols, G. Bauchan, C.T. Chao,and W.M. Jurick. 2016. Wound responses of wild apples suggest multiple resistance mechanism against blue mold. Postharvest Biology & Technology 171:132-140.

Migicovsky Z., K.M. Gardner, D. Money, J. Sawler, J.S. Bloom, P. Moffett, C.T. Chao, H. Schwaninger, G. Fazio, G.-Y. Zhong, and S. Myles. 2016. Genome to phenome mapping in apple using historical data. Plant Genome 9(2) DOI: 10.3835/plantgenome2015.11.0113.

Volk, G.M., A.D. Henk, P.L. Forsline, A.K. Szewc-McFadden, G. Fazio, H. Aldwinckle, and C.M. Richards. 2016. Seeds capture the diversity of genetic resource collections of *Malus sieversii* maintained in an orchard. Genet. Resour. & Crop Evol. doi:10.1007/s10722-016-0450-8

**2017**

Arro J., J. Cuenca, Y. Yang, Z. Liang, P. Cousins, and G.Y. Zhong. 2017. A transcriptome analysis of two grapevine populations segregating for tendril phyllotaxy. Hort, Research 4:17032. doi: 710.1038/hortres.2017.32

Bird, K.A., H. An, E. Gazave, M.A. Gore, J.C. Pires, L.D. Robertson, and J.A. Labate. 2017. Population structure and phylogenetic relationships in a diverse panel of *Brassica rapa* L. Front.Plant Science 8:321. doi: 10.3389/fpls.2017.00321.

Duan N., Y. Bai, H. Sun, N. Wang, C. Jiao, N. Legall, T. He, K. Wang, S. Jiang, H. Xu, Z. Zhang, Z. Mao, Y. Jiang, S. Wu, S. Feng, X. Chen, J. Liu, D. Wang, D. Liu, Y. Wang, C. Yin, W. Zuo, C. Liu, Y. Xu, K. Xu, C.T. Chao, G.-Y. Zhong, L. Cheng, Z. Fei, and X. Chen. 2017. Genomic analyses provide new insights into apple evolution, domestication and genetic diversity. Nature Communication 8:249. <https://www.nature.com/articles/s41467-017-00336-7.pdf>

Khan, A. and T. Chao. 2017. Wild apple species as a source of fire blight resistance for sustainable productivity of apple orchards. Fruit Quarterly 25(4):13 & 15-18.

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Norelli, J.L., M. Wisniewski, G. Fazio, E. Burchard, B. Gutierrez, E. Levin, and S. Droby. 2017. Genotyping-by-sequencing markers facilitate the identification of quantitative trait loci controlling resistance to *Penicillium expansum* in *Malus sieversii*. PlosOone 12(3):e0172949.

Volk, G.M., M.M. Jenderek, and C.T. Chao. 2017. Prioritization of *Malus* accessions for collection cryopreservation at the USDA-ARS national Center for Genetic Resources Preservation. Acta Hort. 1172:267-272.

**2018**

Labate, J.A., A.P. Breksa III, L.D. Robertson, B.A. King, and D.E. King. 2018. Macro-element mineral concentrations in 52 historically important tomato varieties. Plant Genet. Resour. Characterization & Utilization (*in press*).

**APPENDIX C:** Recent (2013-2017) Select Publications of NE-9 Regional Technical Advisory Committee Members**.**

Anderson, N.O., P.D. Ascher, V. Fritz, C. Rohwer, S. Poppe, S. Yao, P. Johnson, B.E. Liedl, J. Reith-Rozelle, L. Klossner, and N. Eash. 2015. Chrysanthemum× hybridum Mammoth™ ‘Dark Bronze Daisy’ garden chrysanthemum. HortScience, 50(8):1260-1264.

Asanidze, Z., M. Akhalkatsi, A.D. Henk, C.M. Richards, and G.M. Volk. 2014. Genetic relationships between wild progenitor pear (*Pyrus* L.) species and local cultivars native to Georgia, South Caucasus. Flora. 209(9):504-512. DOI: 10.1016/j.flora.2014.06.013.

Bai, Y., L. Dougherty, L. Cheng, G. Zhong, and K. Xu. 2015. Uncovering co-expression gene network regulating fruit acidity in diverse apples. BMC Genomics 16(1):612. DOI:10.1186/s12864-015-1816-6.

Paola, B., L. Cadle-Davidson, J. Harriman, J.C. Glaubitz, S. Brooks, K. Hyma, and B. Reisch. 2014. Grapevine powdery mildew resistance and susceptibility loci identified on a high-resolution SNP map. Theor. & Appl. Genet. 127:73-84.

Bassil, N.V., A. Bidani, K.E. Hummer, L.J. Rowland, J. Olmstead, C.M. Richards, and P. Lyrene. 2017. Genetic diversity of wild Southeastern American *Vaccinium* species using microsatellite markers. Genet. Resour. & Crop Evol. doi: 10.1007/s10722-017-0585-2.

Bonina-Noseworthy, J., J.B. Loy, J. Curran-Celentano, R. Sideman, and D.A. Kopsell. 2016. Carotenoid concentration and composition in winter squash: variability associated with different cultigens, harvest maturities, and storage times. HortScience 51:472-480.

Boudreau, T.F., G.M. Peck, S.F. O'Keefe, and A.C. Stewart. 2018. Free amino nitrogen concentration correlates to total yeast assimilable nitrogen concentration in apple juice. Food Science & Nutrition 6:119-123.

Cheong, E.J., C. Kim, G.R. Kinard, and R. Li. 2015. Evaluation of the virus and viroid infection status of flowering cherry (*Prunus yedoensis*) collections in Korea and the United States. J. Plant Pathology. 97:155-160.

DeLong, C.N., S.Y. Keith, L. Combs, R.E. Veilleux, and G.M. Peck. 2016. Apple pollen tube growth rates are regulated by parentage and environment. J. Amer. Soc. Hort. Sci. 141:548-554.

Konstantin, D., P. Barba, L. Cadle-Davidson, and B.I. Reisch. 2018. Single and multiple phenotype QTL analyses of downy mildew resistance in interspecific grapevines. Theor. & Appl. Genet. 1-11.

Dougherty, L., R. Singh, S. Brown, C. Dardick, and K. Xu. 2018. Exploring DNA variant segregation types in pooled genome sequencing enables effective mapping of weeping trait in *Malus*. J. Expt. Bot. doi:10.1093/jxb/erx490

Dougherty, L., Y. Zhu, and K. Xu. 2016. Assessing the allelotypic effect of two aminocyclopropane carboxylic acid synthase-encoding genes MdACS1 and MdACS3a on fruit ethylene production and softening in *Malus*. Horticulture Research 3:16024.

Eicholtz, M.I., S.C. Grinstead, L. Wu, G.R. Kinard, and R. Li. 2017. First report of Beet western yellows virus infecting *Epiphyllum* spp. Plant Disease. https://doi.org/10.1094/PDIS-08-17-1238-PDN.

El-Sharkawy, I., D. Liang, and K. Xu. 2015. Transcriptome analysis of an apple (*Malus× domestica*) yellow fruit somatic mutation identifies a gene network module highly associated with anthocyanin and epigenetic regulation. J. Expt. Bot. 66:7359-7376.

Fazio, G., C.T. Chao, P. Forsline, C.M. Richards, and G.M. Volk. 2014. Tree and root architecture of *Malus sieversii* seedlings for rootstock breeding. Acta Hort. 1058:585-594.

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Gao, Y., F. Liu, K. Wang, D. Wang, X. Gong, L. Liu, C.M. Richards, A.D. Henk, and G.M. Volk. 2015. Genetic diversity of Malus cultivars and wild relatives in the Chinese National Repository of Apple Germplasm Resources. Tree Genetics & Genomes. 11:106. doi:10.1007/s11295-015-0913-7.

Gardner, K.M., P. Brown, T.F. Cooke, S. Cann, F. Costa, C. Bustamante, R. Velasco, M. Troggio, and S. Myles. 2014. Fast and cost-effective genetic mapping in apple using next-generation sequencing. G3: Genes, Genomes, Genetics 4:1681-1687.

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Greene, S.L., C. Khoury, K.A. Williams, J.H. Wiersema, and G.R. Kinard. 2015. Collecting crop wild relatives: an emerging priority. Meeting Abstract. National Native Seed Conference, Santa Fe, NM April 10-13, 2015.

Gross, B.L., A.D. Henk, R.M. Bonnart, and G.M. Volk. 2016. Changes in transcript expression patterns as a result of cryoprotectant treatment and liquid nitrogen exposure in Arabidopsis shoot tips. Plant Cell Reports 36:459-470. doi:10.1007/s00299-016-2095-7.

Grumet, R., Z. Fei, A. Levi, J.D. McCreight, M. Mazourek, M. Palma, J. Schultheis et al. 2016. CucCAP-Developing Genomic Resources for the Cucurbit Community.

Hansen, Z.R., I.M. Small, M. Mutschler, W.E. Fry, and C.D. Smart. 2014. Differential susceptibility of 39 tomato varieties to *Phytophthora infestans* clonal lineage US-23. Plant Disease 98(12):1666-1670.

Hardegree, S.P., C. Moffet, C.T. Walters, R.L. Sheley, and G.N. Flerchinger. 2017. Hydrothermal germination models: Improving experimental efficiency by limiting data collection to the relevant hydrothermal range. Crop Sci. 57:2753-2760. doi:10.2135/cropsci2017.02.0133.

Hart, J.P., and P.D. Griffiths. 2015. Genotyping-by-sequencing enabled mapping and marker development for the by-2 potyvirus resistance allele in common bean. Plant Genome 8:1.

Hoban, S., A. Strand, N. Fraga, C.M. Richards, and S. Schlarbaum. 2015. Developing quantitative seed sampling protocols using simulations: A reply to comments from Guja et al. and Guerrant et al. Biological Conservation. 184:469-470.

Holdsworth, W.L., E. Gazave, P. Cheng, J.R. Myers, M.A. Gore, C.J. Coyne, R.J. McGee, and M. Mazourek. 2017. A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. Horticulture Research 4:17017.

Holdsworth, W.L., K.E. LaPlant, D.C. Bell, M.M. Jahn, and M. Mazourek. 2016. Cultivar-based introgression mapping reveals wild species-derived Pm-0, the major powdery mildew resistance locus in squash. PlosOne 11(12):e0167715.

Hufbauer, R.A., M. Szucs, E. Kasyon, C. Youngberg, M.J. Koontz, C.M. Richards, T. Tuff, and B.A. Melbourne. 2015. Three types of rescue can avert extinction in a changing environment. Proc. Nat. Acad. Sci. 112(33):10557-10562.

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Khoury, C.K., S.L. Greene, K.A. Williams, C. Sosa, and C.M. Richards. 2016. Conservation priorities for tree crop wild relatives in the United States. Symposium Proceedings. Gene Conservation of Tree Species, Chicago, IL. May 16-19, 2016.

Kurtz, B., C.A.C. Gardner, M.J. Millard, T. Nickson, and J.S.C. Smith. 2016. Global access to maize germplasm provided by the US National Plant Germplasm System and by US plant breeders. Crop Sci. 56(3):931-941.

Lalancette, N., D.L. Ward, and J.C. Goffreda. 2014. Susceptibility of peach cultivars to rusty spot and characterization of susceptibility groups. HortScience 49(5):615-621.

Leckie, B.M., D.A. D'Ambrosio, T.M. Chappell, R. Halitschke, D.M. De Jong, A. Kessler, G.G. Kennedy, and M.A. Mutschler. 2016. Differential and synergistic functionality of acylsugars in suppressing oviposition by insect herbivores. PlosOne 11(4):e0153345.

Li, R., G.R. Kinard, D.S. Mollov, M.N. Tahir, P. Lan, and F. Li. 2015. Genetic diversity and population structure of begomoviruses infecting sweet potato. Phytopathology 105:S4.135.

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**Appendix D:** Facilities and Equipment

Facilities

1. PGRU is divided between three buildings located on the campus of the New York State Agriculture Experiment Station, Cornell University, Geneva, New York.
	1. USDA Building (592 m² or 6,372 sq ft) houses the laboratory, administration, components as well as facilities for clonal crops
		1. Five offices (114 m² or 1,227 sq ft), including Research Leader, Computer Specialist, Molecular Biologist, Computer support staff and Administrative Support Staff.
		2. Laboratory Space (157 m2 or 1,690 sq ft )
		3. Three Clonal Greenhouses (160 m2 or 1,722 sq ft)
		4. Headhouse (92 m² or 990 sq ft)
		5. Characterization room (30 m² or 323 sq ft)
		6. Nematode Laboratory (12 m² or 129 sq ft)
		7. Cold Storage (26 m² or 280 sq ft)
	2. Clonal Office Building was finished in July 2001 with 4 scientist offices at 100 sq ft each. Technician room with 10 cubicle workstations for the clonal program technicians and breeding program technicians at 400 sq ft. One unisex bathroom and open storage area.
	3. The Seed Processing Building houses the NERPIS office, seed processing and storage facilities
		1. Office space (858 sq ft), contains three enclosed offices for Vegetable Curator/Horticulturist, Statistician and the Operations Manager. Desk space for Greenhouse Manager, three Agricultural Science Technicians and a Biological Science Aid.
		2. Vernalization chamber (291 sq ft) held at 20 °C and ambient humidity.
		3. Seed cold storage room (47 m2 or 529 sq ft) held at 0° C and 20% relative humidity.
		4. Cold storage anteroom (27 m2 or 330 sq ft) held at 4° C and 30% relative humidity.
		5. Restrooms (47 m2 or 506 sq ft) handicap equipped, separate for male and female.
		6. Conference room-736 sq ft is equipped with an overhead projector, whiteboard, PC, television and VCR for seminars and presentations. Room can be divided to separate conference part from kitchenette. Seating for 26.
		7. Hallway (109 m2 or 1,173 sq ft) used for miscellaneous storage and access area for office.
2. Crop and seed production facilities include approximately 24.1 ha of land and 0.10 ha of greenhouses.
	1. Wellington farm (14 ha or 34.58 acres), is located 1.2 km (about 1 mile) north of the Cornell Agritech campus. The PGRU has a lease-to-own contract with Cornell University. The following site improvements have been made:
		1. Comprehensive field drainage system was installed in 1988.
		2. 1105 m2 (11,895 sq ft) field laboratory which includes a 277 m2 (2,982 sq ft) rodent proof storage area for pollination cages and bee keeping equipment, an 483 m2 (5,200 sq ft) farm equipment storage and workshop area and a 350 m2 (3,768 sq ft) heated field lab for planting, harvesting and seed cleaning operations was built in 1989.
		3. Twenty-five hive apiary on a gravel pad was established in 1992.
		4. Trickle irrigation was installed in 1992. The farm was divided into 8 irrigation zones which can be individually scheduled using electronic timers. The system includes a 18,920 liter (4,000 gallon) water storage tank and an injection fertigation system.
		5. Electrified deer fence was installed in 1992. A deer fence now encloses both the Wellington Farm and the adjacent McCarthy Farm which is used by the NCGR.
		6. 3-sided equipment shed
	2. McCarthy Farm (Approximately 20 ha or 50 acres) is located 1.3 km (about 1 mile) North of the NYSAES Campus. The PGRU maintains a long-term lease with Cornell University for this property.
		1. Comprehensive field drainage system was installed in 1984-85.
		2. Trickle irrigation was installed in 1984-85. There are 9 risers from the system which are normally controlled.
		3. Electrified deer fenced was installed in 1984-85. The fence was modified/extended in

1992 to encompass the Wellington Farm.

* + 1. 4.05 ha (10 acres) are leased from Cornell University on the Station Nursery Farm which is located 0.4 km (0.2 mile) north of the Wellington farm. Site improvements include trickle irrigation and field tile drainage.
	1. Greenhouse Facilities
		1. Design is complete for remodeling clonal germplasm greenhouses (160 m2 or 1,800 sq ft) and construction will commence in 2003.
		2. Construction was completed on two permanent USDA, ARS greenhouses (450 m2 or 5,000 sq ft) in 1992. One house (PGH-1) is equipped with aluminum-framed rolling benches, the other (PGH-2), has sand bed floors to accommodate pollination cages. Both greenhouses contain computerized environmental controls, automated drip irrigation systems, ratio:feeder fertilizer injector, hot water bottom heat for benches and ground beds and 1,000 watt sodium lights and are heated with steam. Approximate capacity is 5,000 1-gallon pots.
		3. Construction was complete in 2002 on a permanent USDA, ARS greenhouse (2,000 sq ft). The house (PGH-3) is equipped with sand bed floors and computerized environmental controls.
		4. Adjoining headhouse (148 m2 or 1,600 sq ft) contains 12.43 m2 (134 sq ft) potting bench space, 11 soil bins (4.5 hl), 2 walk-in vernalization coolers (92 m2 or 990 sq ft), steel shelving (30 m2 or 323 sq ft) for storage, and vented steel chemical storage cabinet for pesticide storage and was completed in 2004.

Information Management

Computer resources include the following offsite server maintained by the Cornell University Computational Biology Service and handle most of our high-throughput genotyping analyses:

* 2x Intel Xeon E5645 2.40GHz (64 GB)
* 4x Intel Xeon E5 4620 v2 2.60GHz (512 GB)
* 8TB (5x2TB HHD @ Raid 5) (1 GB)
* 20TB (6x4TB Raid 6) (10 GB)

We have the following onsite servers for analyses and backup storage:

* CLC Workbench 9 (Intel Xeon E5-2699 2.20GHz 22 Cores) (16 TB) -- Analysis
* Intel Xeon E5-2609 1.9GHz 8TB (5x2TB HHD @ Raid 5) (36.4 TB) -- Storage
* INTEL Core i3-4130 (72 TB) -- Backup Storage

Backups are done in near real time storage server and domain controllers. Additional offsite backups are conducted once every 90 days. The rest of the network computers available consists of approximately 60 desktop PCs running Microsoft Windows 7 with over half workstations running Microsoft Windows 10. All of these have access to the internet, which is provided by Cornell University at a download speed of 530Mbps and upload speed of 630Mbps. USDA network is protected by a physical firewall. Microsoft Windows XP systems are for use with lab equipment and are not allowed on the USDA network. Voice over internet protocol (VoIP) is used as our method of telecommunication.

Field Equipment

Equipment used for field maintenance and distribution of seed and clonal collections are listed below:

|  |  |  |
| --- | --- | --- |
| * 3 pt. hitch Spinner Spreader
 | * Debarder
 | * Rotary mower
 |
| * 4 Bottom Plow
 | * Disk
 | * Rotovator
 |
| * Air blast sprayer
 | * Drill
 | * Seed Counter
 |
| * Air Column (5)
 | * Flatbed trucks (5)
 | * Snowmobile
 |
| * ATV (4)
 | * Forklift
 | * Sprayer
 |
| * Auger
 | * Generator
 | * Straw Mulcher
 |
| * Boom Sprayer 110 gallon
 | * Gravity Separator
 | * Thresher (3)
 |
| * Brush Chopper, 5’
 | * Herbicide Sprayer (2)
 | * Tiller, 42” Rotovator
 |
| * Brush Machine
 | * Mower (2)
 | * Tiller, 68" Rotovator
 |
| * Cargo van
 | * Mower Walk Behind
 | * Tractor (14)
 |
| * Cleaner & Tester Mill Seed
 | * Mulch Layer
 | * Tractor Wagon
 |
| * Clipper (2)
 | * Mulch Transplantor
 | * Trailer (2)
 |
| * Crop care Mulch lifter
 | * Mulcher Pulvi/Teeth Notched
 | * Vegetable Seed Separator (2)
 |
| * Cultivator
 | * Multi-Crop Shredder
 | * Ventilation bin controller
 |
| * Cultivator - Vineyard
 | * Plow Coulter-Chisels SL
 |  |
| * Cutter Mower – Sickle-bar
 | * Power Pruners
 |  |

Laboratory and Characterization Equipment

Equipment used for characterization and research of seed and clonal collections are listed below:

|  |  |  |
| --- | --- | --- |
| * Autoclave
 | * HPLC System
 | * Refractometer (2)
 |
| * Balance (3)
 | * Hybridization oven (2)
 | * Repeater Thin/Thin
 |
| * Calculator, DNA/RNA
 | * Ice machine
 | * Rotor (8)
 |
| * Centrifuge (7)
 | * Incubator (2)
 | * Shaker, Environmental (2)
 |
| * Centrifuge (refrigerated)
 | * Laminar Flow Hood (2)
 | * Shaker, Junior Orbital (2)
 |
| * Cold Chamber (2)
 | * Liquid nitrogen tank
 | * Speedvac (2)
 |
| * Digital imager/Analysis
 | * Lyophilizer system
 | * Still
 |
| * Dishwasher
 | * Microplate Reader
 | * Titrator, automated
 |
| * DJI Phantom Drone
 | * Oven (2)
 | * Transfer lamp
 |
| * Fotosystem 1000
 | * PCR Machine (8)
 | * Tristimulus Colorimeter (3)
 |
| * Freezer, -20℃ (2)
 | * Penetrometer, digital
 | * Uninterrupted Power Supply (2)
 |
| * Freezer, -80℃ (9)
 | * pH meter (2)
 | * Vacuum Centrifuge
 |
| * Genetic Analyzer
 | * Plate reader
 | * Vacuum Manifold
 |
| * GenoGrinder (2)
 | * Printer
 | * Water Filtration System
 |

# APPENDIX E: Project participants for the NE-9 Regional Research Project

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**APPENDIX F:** Projected participation, allocation of resources of state and federal participants for Regional Research Project NE9: Plant Genetic Resources Conservation and Utilization.

|  |  |  |  |
| --- | --- | --- | --- |
| **Participant Name, Email Address and Phone Number** | **Institution and Department** | **Research** | **Objectives** |
| CRIS Codes | Personnel |
| RPA | SOI | FOS | SY | PY | TY | 1 | 2 | 3 | 4 |
| Gan-Yuan ZhongGanYuan.zhong@ars.usda.gov 315-787-2482 | PGRU, USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080 | 0.25 | - | 1.25 |  | X | X | X |
| Benjamin Gutierrezben.gutierrez@ars.usda.gov315-787-2439 | PGRU, USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080 | 1.00 | - | 2.00 | X | X | X | X |
| C. Thomas Chao c.thomas.chao@ars.usda.gov315-787-2454 | PGRU, USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080 | 1.00 | - | 2.60 | X | X | X | X |
| Joanne Labate joanne.labate@ars.usda.gov315-787-2438 | PGRU, USDA, ARS | 202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 1.00 | - | 6.60 |  | X | X | X |
| Peter Bretting peter.bretting@ars.usda.gov 301-504-5541 | NPS, USDA, ARS,National ProgramLeader NP301 | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.10 | - | - | X | X | X | X |
| Gary Kinard gary.kinard@ars.usda.gov 301-504-5951 | National Germplasm Resources Laboratory USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.15 | 1.00 | - | X |  | X |  |

|  |  |  |  |
| --- | --- | --- | --- |
| **Participant Name, Email Address and Phone Number** | **Institution and Department** | **Research** | **Objectives** |
| CRIS Codes | Personnel |
| RPA | SOI | FOS | SY | PY | TY | 1 | 2 | 3 | 4 |
| Karen Williams karen.williams@ ars.usda.gov 301-504-5421 | National Germplasm Resources Laboratory USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.15 | - | 0.15 | X |  |  |  |
| Christina Walters christina.walters@ ars.usda.gov 970-495-3202 | National Center for Genetic Resources Preservation;USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.10 | 0.10 | 0.05 | X |  |  |  |
| Gayle Volkgayle.volk@ars.usda.gov970-492-7607 | National Center for Genetic Resources Preservation;USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.10 | 0.10 | 0.05 | X |  |  |  |
| Christopher Richards christopher.richards@ ars.usda.gov 970-495-3201 | National Center for Genetic Resources Preservation;USDA, ARS | 202-1110-1080; 202-1112-1080202-1130-1080; 202-1131-1080202-1132-1080; 202-1139-1080202-1429-1080; 202-1430-1080202-1451-1080; 202-1460-1080202-1469-1080 | 0.10 | 0.05 | X | X |  |  | X |
| Total SY, PY, TY and FTE | X | X |  |  |  | X | X | X | X |

1 Research Problem Area(s) (RPA), Subject(s) of Investigation (SOI), and Field(s) of Science (FOS) 2 SY = scientist years, PY = professional years, TY = technician years