**Time Line and Key Publications for Horse Gene Mapping and Genomics Workshops**

**1995: First Havemeyer International Horse Gene Mapping Workshop**

**Hosted by Ernie Bailey and Doug Antczak, Lexington Kentucky**

**\*Workshop Goal a 300-marker linkage map**

Key Publication: Raudsepp T, Frönicke L, Scherthan H, Gustavsson I, Chowdhary BP. Zoo-FISH delineates conserved chromosomal segments in horse and man. Chromosome Res. 1996 Apr;4(3):218-25. PubMed PMID: 8793207.

(This publication was part of Terje Raudsepp's doctoral work and demonstrated conservation of genome organization between humans and horses. This work justified the concept of using a horse gene map to leverage data from the human gene map.)

**1996: International Havemeyer workshop on standardization of nomenclature for the domestic horse karyotype**

Bowling AT, Breen M, Chowdhary BP, Hirota K, Lear T, Millon LV, Ponce de Leon FA, Raudsepp T, Stranzinger G. International system for cytogenetic nomenclature of the domestic horse. Report of the Third International Committee for the Standardization of the domestic horse karyotype, Davis, CA, USA, 1996. Chromosome Res. 1997 Nov;5(7):433-43. PubMed PMID: 9421

**1997: Added the Newmarket family to the workshop linkage map**

**1999-2000 Publish first workshop linkage maps**

Guérin G, Bailey E, Bernoco D, Anderson I, Antczak DF, Bell K, Binns MM, Bowling AT, Brandon R, Cholewinski G, Cothran EG, Ellegren H, Förster M, Godard S, Horin P, Ketchum M, Lindgren G, McPartlan H, Mériaux JC, Mickelson JR, Millon LV, Murray J, Neau A, Røed K, Ziegle J, et al. Report of the International Equine Gene Mapping Workshop: male linkage map. Anim Genet. 1999 Oct;30(5):341-54. PubMed PMID: 10582279.

Swinburne J, Gerstenberg C, Breen M, Aldridge V, Lockhart L, Marti E, Antczak D, Eggleston-Stott M, Bailey E, Mickelson J, Røed K, Lindgren G, von Haeringen W, Guérin G, Bjarnason J, Allen T, Binns M. First comprehensive low-density horse linkage map based on two 3-generation, full-sibling, cross-bred horse reference families. Genomics. 2000 Jun 1;66(2):123-34. PubMed PMID: 10860657.

**2001: Third Havemyer Internation al Horse Gene Mapping Workshop**

**Hosted by Kaj Sandberg in Uppsala, Sweden**

**\*Increased the goal of the workshop to 1000 marker linkage maps**

**\*Added Radiation Hybrid Mapping to the workshop program**

**2003: Publish first RH map**

Chowdhary BP, Raudsepp T, Kata SR, Goh G, Millon LV, Allan V, Piumi F, Guérin G, Swinburne J, Binns M, Lear TL, Mickelson J, Murray J, Antczak DF, Womack JE, Skow LC. The first-generation whole-genome radiation hybrid map in the horse identifies conserved segments in human and mouse genomes. Genome Res. 2003 Apr;13(4):742-51. Erratum in: Genome Res. 2003 Jun;13(6a):1258. PubMed PMID: 12671008; PubMed Central PMCID: PMC430160.

**2005- 2006: Publish Second generation linkage maps**

Penedo MC, Millon LV, Bernoco D, Bailey E, Binns M, Cholewinski G, Ellis N, Flynn J, Gralak B, Guthrie A, Hasegawa T, Lindgren G, Lyons LA, Røed KH, Swinburne JE, Tozaki T. International Equine Gene Mapping Workshop Report: a comprehensive linkage map constructed with data from new markers and by merging four mapping resources. Cytogenet Genome Res. 2005;111(1):5-15. PubMed PMID: 16093715.

Swinburne JE, Boursnell M, Hill G, Pettitt L, Allen T, Chowdhary B, Hasegawa T, Kurosawa M, Leeb T, Mashima S, Mickelson JR, Raudsepp T, Tozaki T, Binns M. Single linkage group per chromosome genetic linkage map for the horse, based on two three-generation, full-sibling, crossbred horse reference families. Genomics. 2006 Jan;87(1):1-29. Epub 2005 Nov 28. PubMed PMID: 16314071.

**2005: June: White paper submitted to NHGRI proposing whole genome sequencing for the horse.**

**2005: International Havemeyer Gene Mapping Workshop in Newbridge, Ireland: July 12-14, 2005.**

**\* Adopted whole genome sequencing as a goal of the workshop; Hereafter the workshop is referred to as the "International Havemeyer Horse Genome Workshop"**

**2005: October: NHGRI (Broad Institute) offers to do whole genome sequencing for horse at draft level (2X Sanger sequencing)**

**2005: December: Broad institute selects TWLIGHT as the horse for genome sequencing.**

**2006: February: Sequencing begins on TWILIGHT; Broad decides to do complete level sequencing (6.8X Sanger sequencing)**

**2006: July: Whole genome sequencing of TWILIGHT is completed; Reads available online**

**Fall 2006: First Assembly of Horse Genome (Ecab 1.0)**

**Spring 2007: Second Assembly of Horse Genome (Ecab 2.0)**

Wade CM, Giulotto E, Sigurdsson S, Zoli M, Gnerre S, Imsland F, Lear TL, Adelson DL, Bailey E, Bellone RR, Blöcker H, Distl O, Edgar RC, Garber M, Leeb T, Mauceli E, MacLeod JN, Penedo MC, Raison JM, Sharpe T, Vogel J, Andersson L, Antczak DF, Biagi T, Binns MM, Chowdhary BP, Coleman SJ, Della Valle G, Fryc S, Guérin G, Hasegawa T, Hill EW, Jurka J, Kiialainen A, Lindgren G, Liu J, Magnani E, Mickelson JR, Murray J, Nergadze SG, Onofrio R, Pedroni S, Piras MF, Raudsepp T, Rocchi M, Røed KH, Ryder OA, Searle S, Skow L, Swinburne JE, Syvänen AC, Tozaki T, Valberg SJ, Vaudin M, White JR, Zody MC; Broad Institute Genome Sequencing Platform; Broad Institute Whole Genome Assembly Team, Lander ES, Lindblad-Toh K. Genome sequence, comparative analysis, and population genetics of the domestic horse. Science. 2009 Nov 6;326(5954):865-7. doi: 10.1126/science.1178158. PubMed PMID: 19892987; PubMed Central PMCID: PMC3785132

**2009: SNP test Tool developed for GWAS studies of horses**

McCue ME, Bannasch DL, Petersen JL, Gurr J, Bailey E, Binns MM, Distl O, Guérin G, Hasegawa T, Hill EW, Leeb T, Lindgren G, Penedo MC, Røed KH, Ryder OA, Swinburne JE, Tozaki T, Valberg SJ, Vaudin M, Lindblad-Toh K, Wade CM, Mickelson JR. A high density SNP array for the domestic horse and extant Perissodactyla: utility for association mapping, genetic diversity, and phylogeny studies. PLoS Genet. 2012 Jan;8(1):e1002451. doi: 10.1371/journal.pgen.1002451. Epub 2012 Jan 12. PubMed PMID: 22253606; PubMed Central PMCID: PMC3257288.

Petersen JL, Mickelson JR, Cothran EG, Andersson LS, Axelsson J, Bailey E, Bannasch D, Binns MM, Borges AS, Brama P, da Câmara Machado A, Distl O, Felicetti M, Fox-Clipsham L, Graves KT, Guérin G, Haase B, Hasegawa T, Hemmann K, Hill EW, Leeb T, Lindgren G, Lohi H, Lopes MS, McGivney BA, Mikko S, Orr N, Penedo MC, Piercy RJ, Raekallio M, Rieder S, Røed KH, Silvestrelli M, Swinburne J, Tozaki T, Vaudin M, M Wade C, McCue ME. Genetic diversity in the modern horse illustrated from genome-wide SNP data. PLoS One. 2013;8(1):e54997. doi: 10.1371/journal.pone.0054997. Epub 2013 Jan 30. PubMed PMID: 23383025; PubMed Central PMCID: PMC3559798.

Petersen JL, Mickelson JR, Rendahl AK, Valberg SJ, Andersson LS, Axelsson J, Bailey E, Bannasch D, Binns MM, Borges AS, Brama P, da Câmara Machado A, Capomaccio S, Cappelli K, Cothran EG, Distl O, Fox-Clipsham L, Graves KT, Guérin G, Haase B, Hasegawa T, Hemmann K, Hill EW, Leeb T, Lindgren G, Lohi H, Lopes MS, McGivney BA, Mikko S, Orr N, Penedo MC, Piercy RJ, Raekallio M, Rieder S, Røed KH, Swinburne J, Tozaki T, Vaudin M, Wade CM, McCue ME. Genome-wide analysis reveals selection for important traits in domestic horse breeds. PLoS Genet. 2013;9(1):e1003211. doi: 10.1371/journal.pgen.1003211. Epub 2013 Jan 17. PubMed PMID: 23349635; PubMed Central PMCID: PMC3547851.

**2015: Workshop goal adds Functional Genomics as workshop participants become involved in the international livestock efforts association with FAANG (Functional Annotation of Animal Genomes)**

**2016: 670K SNP assay developed**

Schaefer RJ, Schubert M, Bailey E, Bannasch DL, Barrey E, Bar-Gal GK, Brem G, Brooks SA, Distl O, Fries R, Finno CJ, Gerber V, Haase B, Jagannathan V, Kalbfleisch T, Leeb T, Lindgren G, Lopes MS, Mach N, da Câmara Machado A, MacLeod JN, McCoy A, Metzger J, Penedo C, Polani S, Rieder S, Tammen I, Tetens J, Thaller G, Verini-Supplizi A, Wade CM, Wallner B, Orlando L, Mickelson JR, McCue ME. Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics. 2017 Jul 27;18(1):565. doi: 10.1186/s12864-017-3943-8. PubMed PMID: 28750625; PubMed Central PMCID: PMC5530493.

**2018: Ecab 3.0 produced**