

## Bibliography

- Ashley, C.T., Sutcliffe, J.S., Kunst, C.B., Leiner, H.A., Eichler, E.E., Nelson, D.L. and Warren, S.T. 1993. Human and murine FMR-1 alternative splicing and translational initiation downstream of the CGG repeat. *Nature Genet.* 4: 244-251.
- Bell, M.V., Hirst, M.C., Nakahori, Y., MacKinnon, R.N., Roche, A., Flint, T.J., Jacobs, P.A., Tommerup, N., Tranebjaerg, L., Froster-Iskenius, U., Kerr, B., Turner, G., Lindenbaum, R.H., Winter, R., Pembrey, M., Thibodeau, S., and Davies, K.E. 1991. Physical mapping across the fragile X: hypermethylation and clinical expression of the fragile X syndrome. *Cell.* 64: 861-868.
- Bestor, T. 2000. DNA methyltransferases of mammals. *Hum. Mol. Genet.* 9: 2395-2402.
- Brown, W.T., Houck, G.E. Jr., Jeziorowska, A., Levinson, F.N., Ding, X., Zhong, N., Henderson, J., Brooks, S.S. and Jenkins, E.C. 1993. Rapid fragile X carriers screening and prenatal diagnosis using a non radioactive PCR test. *JAMA.* 270: 1569-1575.
- Brown, W.T. 1996. The molecular biology of the fragile X mutation, p. 88-113. *In* Hagerman, R.J., and Cronister, A. (ed), *Fragile X syndrome: diagnosis, treatment, and research*, 2<sup>nd</sup> ed., the Johns Hopkins University Press, Baltimore.
- Brunberg, J.A., Jacquemont, S., Hagerman, R.J., Berry-Kravis, E., Grigsby, J., Leehey, M.A., Tassone, F., Brown, W.T., Greco, C., and Hagerman, P.J.

2003. Fragile X premutation carriers: characteristic MR Imaging findings of adult male patients with progressive cerebellar and cognitive dysfunction. Am. J. Neuroradiol. 23: 1757-1766.
- Burman, R.W., Yates, P.A., Green, L.D., Jacky, P.B., Turker, M.S., and Popovich, B.W. 1999. Hypomethylation of an expanded *FMR1* allele is not associated with a global DNA methylation defect. Am. J. Hum. Genet. 65: 1375-1386.
- Charalsawad, C. and Limprasert, P. 2000. Rapid and simple sex determination by PCR using *SRY* and *ATLI* primers. Songkla. Med. J. 18: 115-119.
- Chen, X., Santhana Mariappan, S.V., Catasti, P., Ratliff, R., Moyzis, R.K., Laayoun, A., Smith, S.S., Bradbury, E.M., and Gupta G. 1995. Hairpins are formed by the DNA single strands of the fragile X triplet repeats: structure and biological implications. Proc. Natl. Acad. Sci. USA. 92: 5199-5203.
- Chiurazzi, P., Pomponi, M.G., Willemsen, R., Oostra, B.A., and Neri, G. 1998. In vitro reactivation of the *FMR1* gene involved in fragile X syndrome. Hum. Mol. Genet. 7: 109-113.
- Chiurazzi, P., Pomponi, M.G., Pietrobono, R., Bakker, C.E., Neri, G., and Oostra, B.A. 1999. Synergistic effect of histone hyperacetylation and DNA demethylation in the reactivation of the *FMR1* gene. Hum. Mol. Genet. 8: 2317-2323.
- Chong, S.S., Eichler, E.E., Nelson, D.L., and Hughes, M.R. 1994. Robust amplification and ethidium-visible detection of the fragile X syndrome CGG repeat using Pfu polymerase. Am. J. Med. Genet. 51: 522-526.
- Clark, S.J., Harrison, J., Paul, C.L., and Frommer, M. 1994. High sensitivity mapping of methylated cytosine. Nucl. Acids Res. 22: 2990-2997.

- Coffee, B., Zhang, F., Warren, S.T., and Reines, D. 1999. Acetylated histones are associated with FMR1 in normal but not fragile X-syndrome cells. *Nature Genet.* 22: 98-100.
- Comery, T.A., Harris, J.B., Willems, P.J., Oostra, B.A., Irwin, S.A., Weiler, I.J., and Greenough WT. 1997. Abnormal dendritic spines in fragile X knockout mice: maturation and pruning deficits. *Proc. Natl. Acad. Sci. USA.* 94: 5401-5404.
- Condorelli, D.F., Milana, G., Dell'Albani, P., Roccazzello, A.M., Insirello, E., Pavone, L., and Mollica, F. 1996. Routine clinical application of FRAXA Pfu PCR assay: limits and utility. *Clin. Genet.* 50: 366-371.
- Corbin, F., Bouillon, M., Fortin, A., Morin, S., Rousseau, F., and Khandjian, E.W. 1997. The fragile X mental retardation protein is associated with poly (A)+ mRNA in actively translating polyribosomes. *Hum. Mol. Genet.* 6: 1465-1472.
- Costello, J.F., and Plass, C. 2001. Methylation matter. *J. Med. Genet.* 38: 285-303.
- Das, S., Kubota, T., Song, M., Daniel, R., Berry-Kravis, E.M., Prior, T.W., Popovich, P.B., Rosser, L., Arinami, T., and Ledbetter, D.H. 1997/98. Methylation analysis of the fragile X syndrome by PCR. *Genet. Testing.* 1: 151-155.
- de Boulle, K., Verkerk, A.J., Reyniers, E., Vits, L., Hendrickx, J., Van Roy, B., Van den Bos, F., de Graaff, E., Oostra, B.A., and Willems, P.J. 1993. A point mutation in the *FMR-1* gene associated with fragile X mental retardation. *Nature Genet.* 3: 31-35.
- de Varies, B.B., van den Ouwehand, A.M., Mohkamsing, S., Duivenvoorden, H.J., Mol, E., Gelsema, K., van Rijn, M., Halley, D.J.J., Sandkuijl, L.A., Oostra, B.A., Tibben, A., Niermeijer, M.F., and the collaborative fragile X study

- group. 1997. Screening and diagnosis for the fragile X syndrome among the mentally retarded: an epidemiological and Psychological survey. Am. J. Hum. Genet. 61: 660-667.
- Devys, D., Biancalana, V., Boué, R.J., Mandel, J.L., and Obelé, I. 1992. Analysis of full fragile X mutations in fetal tissues and monozygotic twins indicate that abnormal methylation and somatic heterogeneity are established early in development. Am. J. Med. Genet. 43: 208-216.
- Eberhart, D.E., Malter, H.E., Feng, Y., and Warren, S.T. 1996. The fragile X mental retardation protein is a ribonucleoprotein containing both nuclear localization and nuclear export signals. Hum. Mol. Genet. 5: 1083-1091.
- Eichler, E.E., Richards, S., Gibbs, R.A., and Nelson, D.L. 1993. Fine structure of the human *FMR1* gene. Hum. Mol. Genet. 2: 1147-1153.
- Eichler, E.E., Holden, J.J., Popovich, B.W., Reiss, A.L., Snow, K., Thibodeau, S.N., Richards, C.S., Ward, P.A., and Nelson DL. 1994. Length of uninterrupted CGG repeats determines instability in the *FMR1* gene. Nature Genet. 8: 88-94.
- Erster, S.H., Brown, W.T., Goonewardena, P., Dobkin, C.S., Jenkins, E.C., and Pergolizzi, R.G. 1992. Polymerase chain reaction analysis of fragile X mutations. Hum. Genet. 90: 55-61.
- Feil, R., Charlton, J., Bird, A.P., Walter, J., and Reik, W. 1994. Methylation analysis on individuals chromosomes; improved protocol for bisulphate genomic sequencing. Nucleic Acids Res. 22: 695-696.
- Formmer, M., Mc Donald, L.E., Millar, D.S., Collis, C.M., Watt, F., Grigg, G.W., Molloy, P.L., and Paul, C.L. 1992. A genomic sequencing protocol that yields a

- positive displays of 5-methyl cytosine residue in individual DNA strand. Proc. Natl. Acad. Sci. USA. 89: 1827-1831.
- Fu, Y.H., Kuhl, D.P.A., Pizzuti, A., Pieretti, M., Sutcliffe, J.S., Richards, S., Verkerk, A.J.M.H., Holden, J.J.A., Fenwick, R.G., Warren, S.T., Oostra, B.A., Nelson, D.L., and Caskey, C.T. 1991. Variation of the CGG repeat at the fragile X site results in genetic instability: resolution of the Sherman paradox. Cell. 67: 1047-1058.
- Haddad, L.A., Mingroni-netto, R.C., Vienna-Morgante, A.M., Pena, S.D. 1996. A PCR-based test suitable for screening for fragile X syndrome among mentally retarded males. Hum. Genet. 97: 808-812.
- Hagerman, R.J., Hull, C.E., Safanda, J.F., Carpenter, I., Staley, L.W., O'Connor, R.A., Seydel, C., Mazzocco, M.M.M., Snow, K., Thibodeau, S.N., Kuhl, D., Nelson, D.L., Caskey, T., and Taylor, A.K. 1994. High functioning fragile X males: demonstration of an unmethylated fully expanded FMR-1 mutation associated with protein expression. Am. J. Med. Genet. 51:298-308.
- Hagerman, R.J. 1996. Physical and behavioral phenotype, p.3-87. In Hagerman, R.J., and Cronister, A. (ed), Fragile X syndrome: diagnosis, treatment, and research, 2<sup>nd</sup> ed., the Johns Hopkins University Press, Baltimore.
- Hagerman, R.J., Staley, L.S., O'Conner, R., Lugenbeel, K., Nelson, D.L., McLean, S.D., and Taylor, A.K. 1996. Learning-disabled males with a fragile X CGG expansion in the upper premutation size range. Pediatrics. 97: 122-126.
- Hagerman, R.J., Leehey, M., Heinrichs, W., Tassone, F., Wilson, R., Hills, J., Grigsby, J., Gage, B., and Hagerman, P.J. 2001. Intention tremor,

- parkinsonism, and generalized brain atrophy in male carriers of fragile X. Neurology. 57:127-130.
- Hammond, L.S., Marcias, M.M., Tarleton, J.C., and Shashidhar, P.G. 1997. Fragile X syndrome and deletion in FMR1: New case and review of the literature. Am. J. Med. Genet. 72: 430-434.
- Hansen, R. S., Gartler, S.M., Scott C.R., Chen, S., and Laird C.D. 1992. Methylation analysis of CGG sites in the CpG island of the human *FMR1* gene. Hum. Mol. Genet. 1: 571-578.
- Hecimovic, S., Barisic, I., Muller, A., and Petkovic, K. 1997. Expand long PCR for fragile X mutation. Clin.Genet. 52: 147-154.
- Heitz, D., Rousseau, F., Devys, D., Saccone, S., Abderrahim, H., Le Paslier, D., Cohen, D., Vincent, A., Toniolo, D., Della Valle, G., Honhson, S., Schlessinger, D., Oberle, I., and Mandel, J.L. 1991. Isolation of sequences that span the fragile X and identification of the fragile X-related CpG island. Science. 251: 1236-1239.
- Heitz, D., Devys, D., Imbet, G., Kretz, C., and Mandel, J.L. 1992. Inheritance of the fragile X syndrome: size of fragile X premutation is a major determinant of the transition to full mutation. J. Med. Genet. 29: 794-801.
- Herman, J.G., Graff, J.R., Myohanen, S., Nelkin, B.D., and Baylin, S. 1996. Methylation-specific PCR: a novel PCR assay for methylation status of CpG islands. Proc. Natl. Acad. Sci. USA. 9821-9826.
- Herman, J.G., and Baylin, S.B. 1998. Methylation-specific PCR, p.10.6.1-10.6.10. In Dracopoli, N.C., Haines, J.L., Korf, B.R., Moir, D.T., Morton, C.C., Seidman,

- C.E., Seidman, J.G., and Smith, D.R. (eds), Current protocols in human genetics, John Wiley & Sons, Inc. New York.
- Hinds, H.L., Ashley, C.T., Sutcliffe, J.S., Nelson, D.L., Warren, S.T., Housman, D.E., and Schalling, M. 1993. Tissue specific expression of FMR-1 provides evidence for a functional role in fragile X syndrome. *Nature Genet.* 3: 36-43.
- Hinton, V.J., Brown, W.T., Wisniewski, K., and Rudelli, R.D. 1991. Analysis of neocortex in three males with the fragile X syndrome. *Am. J. Med. Genet.* 41: 289-294.
- Hornstra, I.K., Nelson, D.L., Warren, S.T., and Yang T.P. 1993. High resolution methylation analysis of the FMR1 gene trinucleotide repeat region in fragile X syndrome. *Hum. Mol. Genet.* 2: 1659-1665.
- Huber, K.M., Gallagher, S.M., Warren, S.T., and Bear, M.F. 2002. Altered synaptic plasticity in a mouse model of fragile X mental retardation. *Proc. Natl. Acad. Sci. USA.* 99: 7746-7750.
- Iida, T., Nakahori, Y., Tsutsumi O., Taketani Y., and Nakagome, Y. 1994. The CpG island of the FMR-1 gene is methylated differentially among embryonic tissues: implication for prenatal diagnosis. *Hum. Reprod.* 9: 1741-1743.
- Jacquemont, S., Hagerman, R.J., Leehey, M., Grigsby, J., Zhang, L., Brunberg, J.A., Greco, C., Des Portes, V., Jardini, T., Levine, R., Berry-Klavis, E., Brown, W.T., Schaeffer, S., Kissel, J., Tassone, F., and Hagerman, P.J. 2003. Fragile X premutation tremor/ataxia syndrome: molecular, clinical, and neuroimaging correlates. *Am. J. Hum. Genet.* 72: 869-878.
- Kirchgessner, C.U., Warren, S.T., and Willard H.F. 1995. X-inactivation of the FMR1 fragile X mental retardation gene. *J. Med. Genet.* 32: 925-929.

- Kremer, E.J., Pritchard, M., Lynch, M., Yu, S., Holman, K., Baker, E., Warren, S.T., Schlessinger, D., Sutherland, G.R., and Richards, R.I. 1991. Mapping of DNA instability of the fragile X to a trinucleotide repeat sequence p(CGG)n. *Science*. 252: 1711-1714.
- Kunst, C.B., Zerylnick, C., Karickhoff, L., Eichler, E., Bullard, J., Chalifoux, M., Holden, J.J.A., Torroni, A., Nelson, D.L., and Warren, S.T. 1996. FMR1 in global population. *Am. J. Hum. Genet.* 58: 513-522.
- Kubota, T., Das, S., Christian, S.L., Baylin, S.B., Herman, J.G., and Ledbetter, D.H. 1997. Methylation-specific PCR simplifies imprinting analysis. *Nature Genet.* 16: 16-17.
- Laird, C.D. 1987. Proposed Mechanism of Inheritance and Expression of the Human Fragile-X Syndrome of Mental Retardation. *Genetics*. 117: 587-599.
- Latimer, L.J., and Lee, J.S. 1991. Ethidium bromide does not fluoresce when intercalated adjacent to 7-deazaguanine in duplex DNA. *Biol. Chem.* 266: 13849-13851.
- Larsen, L.A., Gronskov, K., Norgaard-Pedersen, B., Brondum-Nielsen, K., Hasholt, L., and Vuust, J. 1997. High-throughput analysis of fragile X (CGG)n alleles in the normal and premutation range by PCR amplification and automated capillary electrophoresis. *Hum. Genet.* 100: 564-568.
- Leehey, M.A., Munhoz, R.P., Lang, A.E., Brunberg, J.A., Grigsby, J., Greco, C., Jacquemont, S., Tassone, F., Lozano, A.M., Hagerman, P.J., and Hagerman, R.J. 2003. The fragile X premutation presenting as essential tremor. *Arch. Neurol.* 60: 117-121.

- Levinson, G., Maddalena, A., Palmer, F.T., Harton, G.L. Bick, D.P., Howard-Peebles, P.N., Black, S.H., Schulman, J.D. 1994. Improved sizing of fragile X CGG repeats by nested polymerase chain reaction. *Am. J. Med. Genet.* 51: 527-534.
- Limprasert, P., Ruangdaraganon, N., Vasiknanonte, P., Sura, T., Jaruratasirikul, S., Sriwongpanich, N., and Sriplung, H. 2000. A clinical checklist for fragile X syndrome: screening of Thai boys with developmental delay of unknown cause. *J Med. Assoc. Thai.* 83: 1260-6.
- Lubs, H.A. 1969. A marker X chromosome. *Am. J. Hum. Genet.* 21: 231-244.
- Martin, J., and Bell, J. A pedigree of mental defect showing sex-linkage. 1943. *Arch. Neurol. Psychiat.* 6: 154-157.
- McConkie-Rosell, A., Lachiewicz, A.M., Spiridigliozi, G.A., Tarleton, J., Schoenwald, S., Phelan, M.C., Goonewardena, P., Ding, X., and Brown, W.T. 1993. Evidence that methylation of the FMR-1 locus is responsible for variable phenotypic expression of the fragile X syndrome. *Am. J. Hum. Genet.* 53:800-809.
- Migeon, B.R. 1992. Concerning the role of X-inactivation and DNA methylation in fragile X syndrome. *Am. J. Med. Genet.* 43: 291-298.
- Morton, J.E., Bunney, S., Webb, T.P., MacDonald, F., Rindl, P.M., and Bullock, S. 1997. Fragile X syndrome is less common than previously estimated. *J. Med. Genet.* 34: 1-5.
- Murray, A., Youings, S., Dennis, N., Latsky, L., Linehan, P., McKechnie, N., Macpherson, J., Pound, M., and Jacobs, P. 1996. Population screening of the FRAXA and FRAXE loci: molecular analyses of boys with learning difficulties and their mothers. *Hum. Mol. Genet.* 5: 727-735.

- Nolin, S.L., Glicksman, A., Houck, G.E., Brown, W.T., and Dobkin, C.S. 1994. Mosaicism in fragile X affected males. *Am. J. Med. Genet.* 51: 509-512.
- Nolin, S.L., Brown, W.T., Glicksman, A., Houck, G.E. Jr., Gargano, A.D., Sullivan, A., Biancalana, V., Brondum-Nielsen, K., Hjalgrim, H., Holinski-Feder, E., Kooy, F., Longshore, J., Macpherson, J., Mandel, J.L., Matthijs, G., Rousseau, F., Steinbach, P., Vaisanen, M.L., von Koskull, H., and Sherman, S.L. 2003. Expansion of the fragile X CGG repeat in female with premutation or intermediate alleles. *Am. J. Hum. Genet.* 72: 454-464.
- Oberlé, I., Rousseau, F., Heitz, D., Kretz, C., Devys, D., Hanauer, A., Boué, J., Bertheas, M.F., and Mandel, J.L. 1991. Instability of a 550-base pair DNA segment and abnormal methylation in fragile X syndrome. *Science*. 52: 1097-1102.
- O'Donnell, W.T., and Warren, S.T. 2002. A decade of molecular studies of fragile X syndrome. *Annu. Rev. Neurosci.* 25: 315–38.
- Orrico, A., Lucia, G., Dotti, M.T., Plewnia, K., Censini, S., and Federico, A. 1998. Mosaicism for full mutation and normal-sized allele of the FMR1 gene: A new case. *Am. J. Med. Genet.* 78:341-344.
- Pai, J.T., Tsai, S.F., Horng, C.J., Chiu, P.C., Cheng, M.Y., Hsiao, K.J., and Wuu, K.D. 1994. Absence of FMR-1 gene expression can be detected with RNA extracted from dried blood specimens. *Hum. Genet.* 93: 488-493.
- Partington, M.W., Moore, D.Y., and Turner, G.M. 1996. Confirmation of early menopause in fragile X carriers. *Am. J. Med. Genet.* 64:370-372.
- Pergolizzi, R.G., Erster, D.H., Goonewardena, P., and Brown, W.T. 1992. Detection of full fragile X mutation. *Lancet*. 339: 271-272.

- Pieretti, M., Zhang, F.P., Fu, Y.H., Warren, S.T., Oostra, B.A., Caskey, C.T., and Nelson, DL. 1991. Absence of expression of the FMR-1 gene in fragile X syndrome. *Cell*. 66: 817-822.
- Pietrobono, R., Pomponi, M.G., Tabolacci, E., Oostra, B.A., Chiurazzi, P., and Neri, G. 2002. Quantitative analysis of DNA demethylation and transcriptional reactivation of the *FMR1* gene in fragile X cells treated with 5-azadeoxycytidine. *Nucleic Acids Res*. 30: 1-8.
- Pietrobono, R., Tabolacci, E., Zalfa, F., Zito, I., Terracciano, A., Moscato, U., Bagni, C., Oostra, B., Chiurazzi, P., Neri, G. 2005. Molecular dissection of the events leading to inactivation of the *FMR1* gene. *Hum. Mol. Genet.* 14: 267-277.
- Reik, W., Kelsey, G., and Walter, J. 1999. Dissecting de novo methylation. *Nature Genet.* 23: 380-382.
- Robertson, K.D., and Wolffe A.P. DNA methylation in health and disease. 2000. *Nature Rev. Genet.* 1: 11-19.
- Rousseau, F., Heitz, D., Biancalana, V., Blumenfeld, S., Kretz, C., Boue, J., Tommerup, N., Van Der Hagen, C., Blanchet, C.D., Croquette, M.F., Gilgenkrantz, S., Jalbert, P., Voelckel, M.A., Oberle, I., and Mandel, J.L. 1991. Direct analysis by DNA analysis of the fragile X syndrome of mental retardation. *N. Engl. J. Med.* 325: 1673-1681.
- Rousseau, F., Robb, L.J., Rouillard, P., and Der Kaloustian, V.M. 1994. No mental retardation in a man with 40% abnormal methylation of the FMR-1 locus and transmission of sperm cell mutation as premutations. *Hum. Mol. Genet.* 3: 927-930.

- Schmucker, B., and Seidel, J. 1999. Mosaicism for a full mutation and a normal size allele in two fragile X male. Am. J. Med. Genet. 84; 221-225.
- Schwartz, C.E., Dean, J., Howard-Peebles, P.N., Bugge, M., Mikkelsen, M., Tommerup, N., Hull, C., Hagerman, R., Holden, J.J., and Stevenson, R.E. 1994. Obstetrical and gynecological complications in fragile X carriers: a multicenter study. Am. J. Med. Genet. 51:400-402.
- Schwemmle, S., de Graaff, E.D., Deissler, H., Gläser, D., Wöhrle, D. Kennerknecht, I., Just, W., Oostra B.A., Dörfler, W., Vogel, W., and Steinbach, P. 1997. Characterization of FMR1 promoter elements by in vivo footprinting analysis. Am J Hum. Genet. 60: 1354-1362.
- Siomi, H., Siomi, M.C., Nussbaum, R.L., and Dreyfuss G. 1993. The protein product of the fragile X gene, FMR1, has characteristics of an RNA-binding protein. Cell. 74: 291-8.
- Siomi, H., Choi, M., Siomi, M.C., Nussbaum, R.L., and Dreyfuss G. 1994. Essential role for KH domains in RNA binding: impaired RNA binding by a mutation in the KH domain of FMR1 that causes fragile X syndrome. Cell. 77: 33-39.
- Smeets, H.J.M., Smits, A.P.T., Verheij, C.E., Theelen, J.P.G., Willemse, R., van de Burgt, I., Hoogeveen, A.T., Oosterwijk, J.C., and Oostra, B.A. 1995. Normal phenotype in two brothers with a full FMR1 mutation. Hum. Mol. Genet. 4: 2103-2108.
- Smiths, A., Smeets, D., Hamel, B., Dreesen, J., de Haan, A., and van Oost, B. 1994. Prediction of mental status in carriers of the fragile X mutation using CGG repeat length. Am. J. Med. Genet. 51: 497-500.

- Steyaert, J., Borghgraef M., Legius, E., and Fryns, J.P. 1996. Molecular intelligence correlations in young fragile X males with a mild CGG repeat expansion in the FMR1 gene. Am. J. Med. Genet. 64: 274-277.
- Stöger, R., Kajimura, T.M., Brown, W.T., and Laird, C.D. 1997. Epigenetic variation illustrated by DNA methylation patterns of the fragile-X gene *FMR1*. Hum. Mol. Genet. 6: 1791-1801.
- Sutcliffe, J. S., Nelson, D.L., Zhang, F., pieretti, M., Caskey, C.T., Saxe, D., and Warren, S.T. 1992. DNA methylation represses *FMR-1* transcription in fragile X syndrome. Hum. Mol. Genet. 1: 397-400.
- Sutherland, G.R. 1977a. Marker X chromosome and mental retardation. N. Engl. J. Med. 296: 1415.
- Sutherland, G.R. 1977b. Fragile sites on human chromosomes: demonstration of their dependence on the type of tissue culture medium. Science. 197: 265-266.
- Sutherland, G.R. 1979. Heritable fragile sites on human chromosomes I. factors affecting expression in lymphocyte culture. Am. J. Hum. Genet. 31: 125-135.
- Sutherland, G.R., Gedeon, A., Donnelly, A., Byard, R.W., Mulley, J.C., Kremer, E., Lynch, M., Pritchard, M., Yu, S., and Richards, R.I. 1991. Prenatal diagnosis of fragile X syndrome by direct detection of the unstable DNA sequence. N. Engl. J. Med. 325: 1720-1722.
- Suzumori, K., Yamauchi, M., Seki, N., Kondo, I., and Hori, T. 1992. Prenatal diagnosis of hypermethylated full fragile X mutation in chorionic villi of male fetus. J. Med. Genet. 30: 785-787.
- Tamanini, F., Meijer, N., Verheij, C., Willems, P.J., Galjaard, H., Oostra, B.A., and Hoogeveen, A.T. 1996. FMRP is associated to the ribosomes via RNA. Hum. Mol. Genet. 5: 809-813.

- Tassone, F., Longshore, J., Zunich, J., Steinbach, P., Salat, U., and Taylor, A.K. 1999. Tissue-specific methylation differences in a fragile X premutation carrier. *Clin Genet.* 55: 346-357.
- Tassone, F., Hagerman, R.J., Loesch, D.A., Lachiwicz, A., Taylor, A.K., and Hagerman, P.J. 2000. Fragile X males with unmethylated, ful mutation trinucleotide repeat expansions have elevated level of messenger RNA. *Am. J. Med. Genet.* 94: 232-236.
- Taylor, A.K., Safanda, J.F., Lugenbeel, K.A., Nelson, D.L., and Hagerman, R.J. 1994. Molecular and phenotypic studies of fragile X males with variant methylation of the *FMR1* gene reveal that the degree of methylation influences clinical severity. *Am. J. Hum. Genet.* 55 (Suppl): A18.
- Taylor, A.K., Tassone, F., Dyer, P.N., Hersch, S.M., Harris, J.F., Greenough, W.T., and Hagerman, R.J. 1999. Tissue heterogeneity of the *FMR1* mutation in high-functioning male with fragile X syndrome. *Am J. Med. Genet.* 84: 233-239.
- Turner, A.M., Robinson, H., Wakes, S., Laing, S.J., Leigh, D., and Turner, G. 1994. Counseling risk figures for fragile X carriers females of varying band sizes for use in predicting the likelihood in retardation in their offspring. *Am. J. Med. Genet.* 51: 458-462.
- Turner, G., Webb, T., Wake, S., and Robinson, H. 1996. Prevalence of the fragile X syndrome. *Am. J. Med. Genet.* 64: 196-197.
- Uzielli, M.L., Guarducci, S., Lapi, E., Cecconi, A., Ricci, U., and Ricotti, G. 1999. Premature ovarian failure (POF) and fragile X premutation females: from POF to fragile X carrier identification, from fragile X carrier diagnosis to POF association data. *Am. J. Med. Genet.* 84:300-303.

- Verheij, C., Bakker, C.E., de Graaff, E., Keulemans, J., Willemse, R., Verkerk, A.J., Galjaard, H., Reuser, A.J., Hoogeveen, A.T., and Oostra BA. 1993. Characterization and localization of the FMR-1 gene product associated with fragile X syndrome. *Nature*. 363: 722-724.
- Verkerk, A.J.M.H., Pieretti, M., Sutcliffe, J.S., Fu, Y.H., Kuhl, D.P.A., Pizzuti, A., Reiner, O., Richards, S., Victoria, M.F., Zhang, F., Eussen, B.E., van Ommen, G.J.B., Blonden, L.A.J., Riggins, G.J., Chastain, J.L., Kunst, C.B., Galjaard, H., Caskey, C.T., Nelson, D.L., Oostra, B.A., and Warren, S.T. 1991. Identification of a gene (*FMR-1*) containing a CGG repeat coincident with a breakpoint cluster region exhibiting length variation in fragile X syndrome. *Cell*. 65: 905-914.
- Vincent, A., Heitz, D., Petie, C., Kretz, C., Obelé, I., and Mendel, J.L. 1991. Abnormal pattern detected in fragile X patients by pulse-field gel electrophoresis. *Nature*. 349: 624-626.
- Weinhäusel, A., and Hass, O.A. 2001. Evaluation of the fragile X (FRAXA) syndrome with methylation-sensitive PCR. *Hum. Genet.* 108: 450-458.
- Willemse, R., Mohkamsing, S., De Vries, B., Devys, D., van den Ouwehand, A., Mandel, J.L., Galjaad, H., and Oostra, B.A. 1995. Rapid antibody test for fragile X syndrome. *Lancet*. 345: 1147-1148.
- Willemse, R., and Oostra, B.A. 2000. FMRP detection assay for the diagnosis of the fragile X syndrome. *Am. J. Med. Genet.* 97:183-188.
- Willemse, R., Bontekoe, C.J., Severijnen, L., Oostra, B.A. 2002. Timing of the absence of FMR1 expression in full mutation chorionic villi. *Hum. Genet.* 110: 601-605.

- Wöhrle, D., Salat, U., Glaser, D., Mucke, J., Meisel-Stosiek, M., Schindler, D., Vogel, W., and Steinbach, P. 1998. Unusual mutations in high functioning fragile X males: apparent instability of expanded unmethylated CGG repeats. *J. Med. Genet.* 35: 103-111.
- Yamauchi, M., Nagata, S., Seki, N., Toyama, Y., Harada, N., Niikawa, N., Masuno, I., Kajii, T., and Hori, T. 1993. Prenatal diagnosis of fragile X syndrome by direct detection of the dynamic mutation due to an unstable DNA sequence. *Clin. Genet.* 44: 169-172.
- Yu, S., Pritchard, M., Kremer, E., Lynch, M., Nancarrow, J., Baker, E., Holman, K., Mulley, J.C., Warren, S.T., Schlessinger, D., Sutherland, G.R., and Richards RI. 1991. Fragile X phenotype characterized by an unstable region of DNA. *Science*. 952: 1179-1181.
- Zhoe, Y., Law, H-Y., Boehm, C-D., Cutting G.R., Ng, I.S.L., and Chong, S.S. 2004. Robust fragile X (CGG)<sub>n</sub> genotype classification using amethylation specific triple PCR assay. *J. Med. Genet.* 41: e.45.