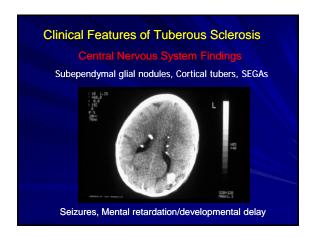
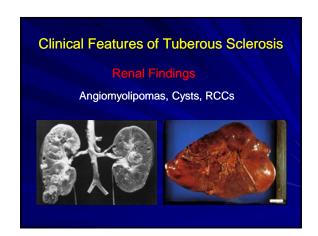


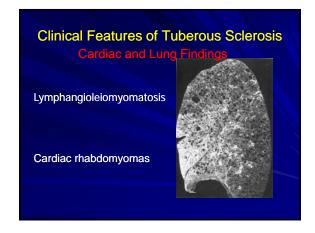
Tuberous Sclerosis Complex (TSC) Autosomal dominant disorder in humans Develop hamartomas (benign tumors resulting from excessive growth of normal tissues) Most frequently affects: skin, brain, kidney, heart and retina Every tissue type of the body can be affected











Frequency of Disease Phenotype Observed Among TSC Patients Phenotype Frequencies Cortical tuber ~90% Facial angiofibroma >80% Renal angiomyolipoma >80% Subependymal nodule ~80% Cardiac rhabdomyomas ~50% Ungual/subungual fibroma 52~88%

Diagnostic Criteria for Tuberous Sclerosis Complex (1998) 11 Major Features Facial angiofibroma, forehead plaques (≥2) Nontraumatic ungual/periungual fibromas (>2) Hypomelianoitic macules (≥3) Shagreen patch (>3) Multiple retinal nodular hamartomas Cortical tuber (>2) Subependymal giant cell astrocytoma (>2) Subependymal giant cell astrocytoma (>2) Cardiac rhabdomyomas Lymphangiomyomas Renal angiomyolipomas Delfinite TSC: 2 major features or 1 major features with 2 minor features Possible TSC: tither 1 major feature or ≥2 minor features Other organs involved: liver, pancreas, thyroid, gonads, arteries, uterus etc.

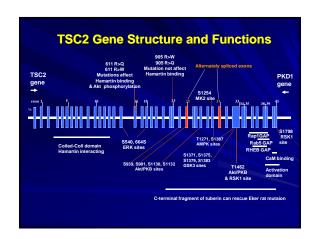
Causes of Premature Death in TSC Patients 13/40 (32.5%) Complications related to severe mental retardation (status epilepticus: bronchpneumonia) 11/40 (27.5%) Renal disease 10/40 (25%) Brain tumors 4/40 (10%) Lymphangiomyomatosis 1/40 (2.5%) Cardiac rhabdomyomas 1/40 (2.5%) Thoracic aneurysm 40/355 (11.3%) Individuals with TSC Followed Long-Term

Genetic Aspects of TSC in 1987 Autosomal dominant inheritance Two-thirds of cases sporadic One-third of cases familial Variable expression Common in the population with approximately 1:6,000-10,000 individuals affected

Identification and characterization of the tuberous sclerosis gene on chromosome 16.

The European Chromosome 16 Tuberous Sclerosis Consortium

Cell 75: 1305 – 1315, 1993.



Identification of the tuberous sclerosis gene TSC1 on chromosome 9q34.

van Slegtenhorst M, de Hoogt R, Hermans C, Nellist M, Janssen B, Verhoef S, Lindhout D, van den Ouweland A, Halley D, Young J, Burley M, Jeremiah S, Woodward K, Nahmias J, Fox M, Ekong R, Osborne J, Wolfe J, Povey S, Snell RG, Cheadle JP, Jones AC, Tachataki M, Ravine D, Sampson JR, Reeve MP, Richardson P, Wilmer F, Munro C, Hawkins TL, Sepp T, Ali JBM, Ward S, Green AJ, Yates JRW, Kwiatkowska J, Hanske EP, Short MP, Haines JH, Jozwiak S, Kwiatkowski DJ.

Science 277: 805 - 808, 1997.

TSC1 Gene Structure and Functions

CDK1/Cyclin B sites

T417 SS84

Alternately spliced exons (UTR)

exons (UTR)

Exons Colled coil domain
Tuberin binding domain
Activate RHO-GTPase

Ref. Lamb et al. 2000. Nat. Cell. Biol. 2-281-6. Hodges et al. 2001. HMG 10-2893-2905. Haddad et a. 2002. JBC 277-44180-6.

~85% of affected individuals have identifiable TSC1 or TSC2 gene mutation

- TSC1 – over 95% protein truncating

- TSC2 – ~25% missense and ~70% protein truncating, ~5% large gene deletion/duplication

Remainder of mutations likely represent:

- Somatic mosaicism

- Mutations in unanalyzed gene regions

- Additional loci?

