

Floating-Harbor Syndrome

<https://www.ncbi.nlm.nih.gov/books/NBK114458/>

SummaryClinical characteristics.Floating-Harbor syndrome (FHS) is characterized by typical craniofacial features; low birth weight, normal head circumference, and short stature; bone age delay that normalizes between ages six and 12 years; skeletal anomalies (brachydactyly, clubbing, clinodactyly, short thumbs, prominent joints, clavicular abnormalities); severe receptive and expressive language impairment; hypernasality and high-pitched voice; and intellectual disability that is typically mild to moderate. Difficulties with temperament and behavior that are present in many children tend to improve in adulthood. Other features can include hyperopia and/or strabismus, conductive hearing loss, seizures, gastroesophageal reflux, renal anomalies (e.g., hydronephrosis / renal pelviectasis, cysts, and/or agenesis), and genital anomalies (e.g., hypospadias and/or undescended testes).

Diagnosis/testing.The diagnosis is established by identification of a heterozygous SRCAP pathogenic variant in those with clinical findings of FHS.

Management.Treatment of manifestations: Early intervention programs, special education, and vocational training to address developmental disabilities; communication rehabilitation with sign language or alternative means of communication; and behavior management by a behavioral specialist/psychologist with consideration of medication as needed. Referral to an endocrinologist for consideration of human growth hormone (HGH) therapy; however, data on use of HGH in FHS are limited. Standard treatment for refractive errors and strabismus, hearing loss, seizures, gastroesophageal reflux, and renal and genitourinary anomalies.

Surveillance: Close monitoring of growth, especially in the first year. Annual: ophthalmologic evaluation, hearing screening, blood pressure measurement, and assessment of renal function. Sonographic evaluation for renal cysts in teenage/adult years is indicated.

Genetic counseling.FHS is inherited in an autosomal dominant manner. The majority of affected individuals have a de novo pathogenic variant. Each child of an individual with FHS has a 50% chance of inheriting the pathogenic variant. Prenatal testing is possible for families in which the pathogenic variant has been identified.

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Diagnosis
Suggestive Findings
Floating-Harbor syndrome (FHS) should be suspected in individuals with the following clinical and radiographic features.
Craniofacial appearance (see Figure 1)
Figure 1. Facial appearance of a girl age 11 years with FHS (SRCAP pathogenic variant p.Arg2444Ter) A. Note triangular face with deep-set eyes; short philtrum; long nose with narrow bridge and broad base with low-hanging columella; and thin upper lip.
Triangular face
Deep-set eyes
Short philtrum
Wide mouth with a thin vermilion border of the upper lip
Long nose with a narrow bridge, broad base, broad tip, and low-hanging columella
Low-set ears

Other features

Significant delay in bone age (<2 SD below the mean) with normalization between ages six and 12 years
Skeletal anomalies. Brachydactyly, broad fingertips that give the appearance of clubbing, clinodactyly, short thumbs, prominent joints, clavicular abnormalities (See Figure 2.)
Short adult stature. 140-155 cm (See Figure 3.)
Figure 2. Dorsal (A) and palmar (B) view of the hands of the girl in Figure 1. Note clinodactyly, widened fingertips, and prominent joints. Figure 3. Frontal view of the girl in Figure 1. She has proportionate short stature with height <3rd centile.

Speech and language

Dysarthria and verbal dyspraxia with phoneme imprecision
Hypernasality
High-pitched voice
Severe receptive and expressive language impairment across all domains of function
Intellectual disability.
All individuals have some degree of intellectual impairment and/or learning disability ranging from borderline normal to moderate intellectual disability.
Establishing the Diagnosis
The diagnosis of FHS is established in a proband with Suggestive Findings by identification of a heterozygous pathogenic (or likely pathogenic) variant in SRCAP on molecular genetic testing (see Table 1).
Note: (1) Per ACMG/AMP variant interpretation guidelines, the terms "pathogenic variants" and "likely pathogenic variants" are synonymous in a clinical setting, meaning that both are considered diagnostic and both

can be used for clinical decision making [Richards et al 2015]. Reference to "pathogenic variants" in this section is understood to include any likely pathogenic variants. (2) Identification of a heterozygous SRCAP variant of uncertain significance does not establish or rule out the diagnosis. Molecular genetic testing approaches can include a combination of gene-targeted testing (single-gene testing, multigene panel) and comprehensive genomic testing (exome sequencing, genome sequencing) depending on the phenotype. Gene-targeted testing requires that the clinician determine which gene(s) are likely involved, whereas genomic testing does not. Because the phenotype of FHS is broad, individuals with the distinctive findings described in Suggestive Findings are likely to be diagnosed using gene-targeted testing (see Option 1), whereas those with a phenotype indistinguishable from many other inherited disorders with short stature and/or intellectual disability are more likely to be diagnosed using genomic testing (see Option 2).

Option 1 When the phenotypic and laboratory findings suggest the diagnosis of FHS, molecular genetic testing approaches can include single-gene testing or use of a multigene panel.

Single-gene testing. Sequence analysis of SRCAP detects small intragenic deletions/insertions and missense, nonsense, and splice site variants; typically, exon or whole-gene deletions/duplications are not detected. Perform sequence analysis first. If no pathogenic variant is found, perform gene-targeted deletion/duplication analysis to detect intragenic deletions or duplications. A multigene panel that includes SRCAP and other genes of interest (see Differential Diagnosis) is most likely to identify the genetic cause of the condition while limiting identification of variants of uncertain significance and pathogenic variants in genes that do not explain the underlying phenotype. Note: (1) The genes included in the panel and the diagnostic sensitivity of the testing used for each gene vary by laboratory and are likely to change over time. (2) Some multigene panels may include genes not associated with the condition discussed in this GeneReview. (3) In some laboratories, panel options may include a custom laboratory-designed panel and/or custom phenotype-focused exome analysis that includes genes specified by the clinician. (4) Methods used in a panel may include sequence analysis, deletion/duplication analysis, and/or other non-sequencing-based tests. For an introduction to multigene panels click [here](#). More

detailed information for clinicians ordering genetic tests can be found [here](#). Option 2 When the phenotype is indistinguishable from many other inherited disorders characterized by short stature, comprehensive genomic testing (which does not require the clinician to determine which gene[s] are likely involved) is the best option. Exome sequencing is most commonly used; genome sequencing is also possible. For an introduction to comprehensive genomic testing [click here](#). More detailed information for clinicians ordering genomic testing can be found [here](#). Epigenetic signature analysis / methylation array. A distinctive epigenetic signature (disorder-specific genome wide changes in DNA methylation profiles) in peripheral blood leukocytes has been identified in individuals with FHS [Aref-Eshghi et al 2019, Aref-Eshghi et al 2020, Levy et al 2021]. Epigenetic signature analysis of a peripheral blood sample or DNA banked from a blood sample can therefore be considered to clarify the diagnosis in individuals with: (1) suggestive findings of FHS but in whom no pathogenic variant in SRCAP has been identified via sequence analysis or genomic testing; or (2) suggestive findings of FHS and a SRCAP variant of uncertain clinical significance identified by molecular genetic testing. For an introduction to epigenetic signature analysis [click here](#).

Table 1. Molecular Genetic Testing Used in Floating-Harbor Syndrome

Gene	Method	Proportion of Probands with a Pathogenic Variant Detectable by Method
SRCAP	Sequence analysis	373/73 individuals
	Gene-targeted deletion/duplication analysis	Unknown

SRCAP

Sequence analysis; 373/73 individuals; 4 Gene-targeted deletion/duplication analysis; 5 Unknown; 61. See Table A. Genes and Databases for chromosome locus and protein. 2. See Molecular Genetics for information on variants detected in this gene. 3. Sequence analysis detects variants that are benign, likely benign, of uncertain significance, likely pathogenic, or pathogenic. Variants may include small intragenic deletions/insertions and missense, nonsense, and splice site variants; typically, exon or whole-gene deletions/duplications are not detected. For issues to consider in interpretation of sequence analysis results, [click here](#). 4. Hood et al [2012], Le Goff et al [2013], Nikkel et al [2013], Dong et al [2014], Kehrer et al [2014], Nagasaki et al [2014], Seifert et al [2014], Amita et al [2016], Coughlin et al [2017], Singh et al [2017], Budisteanu et al

[2018], Choi et al [2018], Milani et al [2018], Shields et al [2019]5. Gene-targeted deletion/duplication analysis detects intragenic deletions or duplications. Methods used may include a range of techniques such as quantitative PCR, long-range PCR, multiplex ligation-dependent probe amplification (MLPA), and a gene-targeted microarray designed to detect single-exon deletions or duplications.6. To date, large deletions that encompass SRCAP have not been associated with FHS phenotype [Author, personal communication] (see Genotype-Phenotype Correlations).

Suggestive FindingsFloating-Harbor syndrome (FHS) should be suspected in individuals with the following clinical and radiographic features.**Craniofacial appearance** (see Figure 1)Figure 1. Facial appearance of a girl age 11 years with FHS (SRCAP pathogenic variant p.Arg2444Ter) A. Note triangular face with deep-set eyes; short philtrum; long nose with narrow bridge and broad base with low-hanging columella; and thin upper lip.Triangular faceDeep-set eyesShort philtrumWide mouth with a thin vermilion border of the upper lipLong nose with a narrow bridge, broad base, broad tip, and low-hanging columellaLow-set ears

Other features

Significant delay in bone age (≥2 SD below the mean) with normalization between ages six and 12 yearsSkeletal anomalies. Brachydactyly, broad fingertips that give the appearance of clubbing, clinodactyly, short thumbs, prominent joints, clavicular abnormalities (See Figure 2.)Short adult stature. 140-155 cm (See Figure 3.)Figure 2. Dorsal (A) and palmar (B) view of the hands of the girl in Figure 1. Note clinodactyly, widened fingertips, and prominent joints. Figure 3. Frontal view of the girl in Figure 1. She has proportionate short stature with height <3rd centile.

Speech and language

Dysarthria and verbal dyspraxia with phoneme imprecisionHypernasalityHigh-pitched voiceSevere receptive and expressive language impairment across all domains of functionIntellectual disability. All individuals have some degree of intellectual impairment and/or learning disability ranging from borderline normal to moderate intellectual disability.

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Figure 3. Frontal view of the girl in Figure 1. She has proportionate short stature with height <3rd centile.

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Hypernasality

High-pitched voice

Severe receptive and expressive language impairment across all domains of function

Establishing the DiagnosisThe diagnosis of FHS is established in a proband with Suggestive Findings by identification of a heterozygous pathogenic (or likely pathogenic) variant in SRCAP on molecular genetic testing (see Table 1).Note: (1) Per ACMG/AMP variant interpretation guidelines, the terms "pathogenic variants" and "likely pathogenic variants" are synonymous in a clinical setting, meaning that both are considered diagnostic and both can be used for clinical decision making

[Richards et al 2015]. Reference to "pathogenic variants" in this section is understood to include any likely pathogenic variants. (2) Identification of a heterozygous SRCAP variant of uncertain significance does not establish or rule out the diagnosis. Molecular genetic testing approaches can include a combination of gene-targeted testing (single-gene testing, multigene panel) and comprehensive genomic testing (exome sequencing, genome sequencing) depending on the phenotype. Gene-targeted testing requires that the clinician determine which gene(s) are likely involved, whereas genomic testing does not. Because the phenotype of FHS is broad, individuals with the distinctive findings described in Suggestive Findings are likely to be diagnosed using gene-targeted testing (see Option 1), whereas those with a phenotype indistinguishable from many other inherited disorders with short stature and/or intellectual disability are more likely to be diagnosed using genomic testing (see Option 2).

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detailed information for clinicians ordering genetic tests can be found [here](#). Option 2 When the phenotype is indistinguishable from many other inherited disorders characterized by short stature, comprehensive genomic testing (which does not require the clinician to determine which gene[s] are likely involved) is the best option. Exome sequencing is most commonly used; genome sequencing is also possible. For an introduction to comprehensive genomic testing [click here](#). More detailed information for clinicians ordering genomic testing can be found [here](#). Epigenetic signature analysis / methylation array. A distinctive epigenetic signature (disorder-specific genome wide changes in DNA methylation profiles) in peripheral blood leukocytes has been identified in individuals with FHS [Aref-Eshghi et al 2019, Aref-Eshghi et al 2020, Levy et al 2021]. Epigenetic signature analysis of a peripheral blood sample or DNA banked from a blood sample can therefore be considered to clarify the diagnosis in individuals with: (1) suggestive findings of FHS but in whom no pathogenic variant in SRCAP has been identified via sequence analysis or genomic testing; or (2) suggestive findings of FHS and a SRCAP variant of uncertain clinical significance identified by molecular genetic testing. For an introduction to epigenetic signature analysis [click here](#).

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Option 2When the phenotype is indistinguishable from many other inherited disorders characterized

by short stature, comprehensive

genomic testing (which does not require the clinician to determine which gene[s] are likely involved) is the best option. Exome sequencing is most commonly used; genome sequencing is also possible. For an introduction to comprehensive genomic testing click [here](#). More detailed information for clinicians ordering genomic testing can be found [here](#). Epigenetic signature analysis / methylation array. A distinctive epigenetic signature (disorder-specific genome wide changes in DNA methylation profiles) in peripheral blood leukocytes has been identified in individuals with FHS [Aref-Eshghi et al 2019, Aref-Eshghi et al 2020, Levy et al 2021]. Epigenetic signature analysis of a peripheral blood sample or DNA banked from a blood sample can therefore be considered to clarify the diagnosis in individuals with: (1) suggestive findings of FHS but in whom no pathogenic variant in SRCAP has been identified via sequence analysis or genomic testing; or (2) suggestive findings of FHS and a SRCAP variant of uncertain clinical significance identified by molecular genetic testing. For an introduction to epigenetic signature analysis click [here](#).

Gene	Method	Proportion of Probands with a Pathogenic Variant	Detectable by Method
SRCAP	Sequence analysis	373/73 individuals	4
	Gene-targeted deletion/duplication analysis	Unknown	61

1. See Table A. Genes and Databases for chromosome locus and protein. 2. See Molecular Genetics for information on variants detected in this gene. 3. Sequence analysis detects variants that are benign, likely benign, of uncertain significance, likely pathogenic, or pathogenic. Variants may include small intragenic deletions/insertions and missense, nonsense, and splice site variants; typically, exon or whole-gene deletions/duplications are not detected. For issues to consider in interpretation of sequence analysis results, click [here](#). 4. Hood et al [2012], Le Goff et al [2013], Nikkel et al [2013], Dong et al [2014], Kehrer et al [2014], Nagasaki et al [2014], Seifert et al [2014], Amita et al [2016], Coughlin et al [2017], Singh et al [2017], Budisteanu et al [2018], Choi et al [2018], Milani et al [2018], Shields et al [2019] 5. Gene-targeted deletion/duplication analysis detects intragenic deletions or duplications. Methods used may include

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a range of techniques such as quantitative PCR, long-range PCR, multiplex ligation-dependent probe amplification (MLPA), and a gene-targeted microarray designed to detect single-exon deletions or duplications.⁶ To date, large deletions that encompass SRCAP have not been associated with FHS phenotype [Author, personal communication] (see Genotype-Phenotype Correlations).

Table 1. Molecular Genetic Testing Used in Floating-Harbor Syndrome
Gene:1MethodProportion of Probands with a Pathogenic Variant:2 Detectable by Method

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Clinical Characteristics
Clinical Description
Prior to the molecular characterization of Floating-Harbor syndrome (FHS) by Hood et al [2012], a number of reports included descriptions of individuals in whom the diagnosis of FHS could be questioned. This GeneReview only includes information on those 73 individuals with molecularly confirmed FHS (i.e., presence of a heterozygous SRCAP pathogenic variant) [Hood et al 2012, Le Goff et al 2013, Nikkel et al 2013, Dong et al 2014, Kehrer et al 2014, Nagasaki et al 2014, Seifert et al 2014, Amita et al 2016, Coughlin et al 2017, Singh et al 2017, Budisteanu et al 2018, Choi et al 2018, Milani et al 2018, Shields et al 2019]. The 41 females and 32 males range in age from eight months to 52 years. FHS is frequently recognized in early childhood because of the characteristic facial features (Figure 1). Infants and younger children are often referred for assessment of poor growth or developmental (predominantly speech and language) delay. Craniofacial features include triangular face, deep-set eyes, short philtrum, wide mouth with a thin vermilion border of the upper lip, long nose with a narrow bridge, broad base, broad tip, and low-hanging columella, and low-set ears. The features become more pronounced with age, especially the length of the nose and the width of the nasal tip. **Intellect.** Although gross motor and fine motor milestones are within normal limits, affected individuals typically have mild-to-moderate intellectual disability. A disorder of speech and language is the most severe disability. Most aspects of communication are affected; expressive language is most consistently and severely affected. Dysarthria and verbal dyspraxia with phoneme imprecision is most common, with absent speech in some individuals. Voice is described as hypernasal and high-pitched. The majority of affected children receive mainstream education with individualized educational plans. **Regression of skills** is not typical of FHS. **Behavior.** Many individuals with FHS have temperament and behavior differences and difficulties: temper tantrums in infancy and

attention-deficit/hyperactivity disorder spectrum with impulsivity, inattention, and restlessness at school age. Aggressive and violent outbursts can occur. Obsessive compulsive disorder and anxiety have been observed. Behavior problems are reported to improve in adulthood. Growth. Short stature is a cardinal sign of FHS. The majority of individuals with FHS have low birth weight (from 3 SD below the mean to 0 SD) and normal head circumference (2 SD below the mean to 0 SD). In the first years of life weight gain and linear growth are poor. A significant delay in bone age is reported (≥2 SD below the mean) with normalization between ages six and 12 years. Average adult height is 140-155 cm. Puberty. Early puberty has been reported; data are insufficient to determine the incidence in either sex. Eye. Five of 73 individuals have been reported with hyperopia and eight of 13 with strabismus. One individual had anterior chamber abnormalities. Hearing. Conductive hearing loss has been seen in eleven of 73 individuals with FHS. Cochlear abnormality has been observed in one of 73. Neurologic. Seizures have been observed in seven of 73 individuals. Gastrointestinal. Reflux can be severe, requiring G-tube feeding in some. Constipation and colonic strictures have been observed. One of 73 individuals had celiac disease; two had transient gluten intolerance. Genitourinary. Renal and genitourinary anomalies can occur and include hypospadias and undescended testes, epididymal cysts, varicocele, and posterior urethral valves in boys. Hydronephrosis/renal pelviectasis and nephrocalcinosis, renal cysts, and renal agenesis have been observed. One adult of the 73 reported individuals developed polycystic kidney disease and end-stage renal disease. Orthopedic. The body habitus is often stocky with a broad chest and short neck. Additional features include hand anomalies such as clinodactyly, brachydactyly, short thumbs, and broad fingertips that give the appearance of clubbing (Figure 2). Clavicular anomalies including pseudarthrosis and clavicular hypoplasia have been observed, as have short metacarpals, 11 pairs of ribs, kyphoscoliosis, prominent joints, dysplastic hips, and dislocated radial heads. Perthes disease has also been reported. Dental. A number of individuals with FHS have dental problems (e.g., caries, microdontia, oligodontia, delayed loss of primary teeth) and orthodontic problems (e.g., maxillary retrusion, underbite). Cardiac. Cardiac malformations are not usually a feature of FHS. Of 73 affected individuals one had mild aortic coarctation, one had mesocardia with persistent left

superior vena cava, two had atrial septal defect, and one individual had tetralogy of Fallot.

Genotype-Phenotype Correlations

Pathogenic variants in exons 33 and 34 of SRCAP that are predicted to cause truncation of the protein (removing 3 C-terminal AT-hook DNA-binding motifs while leaving the CBP-binding and ATPase domains intact) result in the FHS phenotype.

Prevalence

The prevalence of FHS is not known. Seventy-three individuals with a heterozygous SRCAP pathogenic variant have been reported to date [Hood et al 2012, Le Goff et al 2013, Nikkel et al 2013, Dong et al 2014, Kehrer et al 2014, Nagasaki et al 2014, Seifert et al 2014, Amita et al 2016, Coughlin et al 2017, Singh et al 2017, Budisteanu et al 2018, Choi et al 2018, Milani et al 2018, Shields et al 2019]. The majority of individuals reported with FHS are of European origin, but FHS has also been diagnosed in individuals of Chinese, South American, South Asian, Japanese, and Korean background [Hood et al 2012, Nikkel et al 2013, Nagasaki et al 2014, Amita et al 2016, Singh et al 2017, Choi et al 2018]. Whether the occurrence of FHS is lower in nonwhite populations or the observed difference is the result of other factors is not known.

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Craniofacial features

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Genetically Related (Allelic) Disorders SRCAP truncating variants upstream of exon 33 and 34 have been identified in individuals with developmental and health issues, without clinical features of

Floating-Harbor syndrome [Author, personal communication].

Differential Diagnosis The distinctive facial features, bone age delay, and characteristic speech disability that make the diagnosis of Floating-Harbor syndrome (FHS) straightforward in early childhood become less distinct with age. Table 2 lists genes and associated conditions that should be considered in children in whom the diagnosis of FHS is suspected.

Table 2. Other Genes of Interest in the Differential Diagnosis of Floating-Harbor Syndrome (FHS)

View in own window

Gene(s)	Differential Disorder	MOI	Clinical Features of Differential Disorder
CCDC8	Overlapping w/FHS		Distinguishing from FHS
CUL7			
OBSL1			

Three M syndrome

AR

Triangular face
Short 5th fingers
Bone age may be slightly delayed.
Males may have hypospadias.
Severe pre- & postnatal growth restriction (final height 5-6 SD below mean; i.e., 120-130 cm)

Relatively large head, hypoplastic midface, thick eyebrows, fleshy nasal tip, long philtrum, prominent mouth & lips, pointed chin
Normal intelligence
Absence of language impairment
Characteristic radiologic findings
Short broad neck, prominent trapezii, deformed sternum, short thorax, square shoulders, winged scapulae, & hyperlordosis, prominent heels, loose joints
Hypogonadism in males

CREBBP

EP300

Rubinstein-Taybi syndrome

AD

Facial features (e.g., low-hanging columella) Broad or angulated thumbs 5th-finger clinodactyly Short stature

Round face, downslanted palpebral fissures, small mouth opening Severe intellectual disability Normal bone age Cardiac malformations

FOXP2

FOXP2 speech and language disorders

See footnote 2.

Dysarthria Hypernasality Severe expressive & receptive language & literacy impairments

Absence of:

Short stature Delayed bone age FHS characteristic facies Aggression in childhood

Multiple etiologies^{1,3}

Silver-Russell syndrome (SRS) See footnote 3.

Pre- & postnatal growth restriction Expressive language impairment (much more severe in FHS than in SRS)

Body asymmetry Café-au-lait macules Blue sclera Absence of FHS characteristic facial features & thumb anomalies

AR = autosomal recessive; MOI = mode of inheritance; SD = standard deviation(s); SRS =

Silver-Russell syndrome 1. Genes are listed in alphabetic order. 2. Recurrence risk for sibs of

proband with a FOXP2 speech and language disorder depends on the causative genetic alteration.3. Silver-Russell syndrome (SRS) has multiple etiologies including: epigenetic changes that modify expression of genes in the imprinted region of chromosome 11p15.5, maternal UPD7, and (infrequently) autosomal dominant or autosomal recessive inheritance. When a proband has SRS as the result of paternal hypomethylation at IC1 or maternal UPD7, both parents are predicted to be unaffected, the risk to the sibs is not increased over that of the general population, and the risk to offspring is probably low.

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AR = autosomal recessive; MOI = mode of inheritance; SD = standard deviation(s); SRS = Silver-Russell syndrome¹. Genes are listed in alphabetic order.² Recurrence risk for sibs of proband with a FOXP2 speech and language disorder depends on the causative genetic alteration.³ Silver-Russell syndrome (SRS) has multiple etiologies including: epigenetic changes that modify expression of genes in the imprinted region of chromosome 11p15.5, maternal UPD7, and (infrequently) autosomal dominant or autosomal recessive inheritance. When a proband has SRS as the result of paternal hypomethylation at IC1 or maternal UPD7, both parents are predicted to be unaffected, the risk to the sibs is not increased over that of the general population, and the risk to offspring is probably low.

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ManagementEvaluations Following Initial DiagnosisTo establish the extent of disease and needs in an individual diagnosed with Floating-Harbor syndrome (FHS), the evaluations summarized in Table 3 (if not performed as part of the evaluation that led to the diagnosis) are recommended.Table 3.

Recommended Evaluations Following Initial Diagnosis in Individuals with Floating-Harbor

SyndromesView in own windowSystem/ConcernEvaluationComment

Constitutional

Measurement of growth & plotting of growth parametersSyndrome-specific charts are currently not available for children w/a SRCAP pathogenic variant.

Eyes

Ophthalmologic exam

ENT

Audiology eval(See Hereditary Hearing Loss and Deafness Overview for details of eval.)Dental eval

Genitourinary

Renal ultrasound examBlood pressure assessmentAssessment for cryptorchidism in males

Musculoskeletal

Orthopedic assessmentEval for hip dysplasia & clavicular anomalies

Other

Multidisciplinary developmental evalIncl assessment of gross & fine motor skills, speech/language, cognitive abilities, & vocational skills w/special attn to speech delay & anomaliesConsultation w/clinical geneticist &/or genetic counselorTreatment of ManifestationsTreatment includes the following:Early intervention programs, special education, and vocational training to address developmental disabilitiesCommunication rehabilitation with sign language or alternative means of communicationBehavior management strategies including referral to a behavioral specialist/psychologist and consideration of medication if neededReferral of the family to support groups and other resourcesStandard treatment for any of the following if identified:Refractive errors and strabismusHearing lossSeizuresRenal diseaseCryptorchidismOrthopedic complicationsDental problemsReferral to an endocrinologist for consideration of human growth hormone (HGH) therapy. HGH therapy with modest response has been reported in three children with FHS. Caution is

indicated as limited information about HGH therapy in FHS is available. Investigation for celiac disease if indicated by clinical features
Surveillance Table 4. Recommended Surveillance for Individuals with Floating-Harbor Syndrome

View in own window
System/Concern Evaluation Frequency

Constitutional

Eval of growth Close monitoring w/each visit, esp in 1st yr of life

Bone age exam Eval for signs of early puberty

Especially in persons treated w/growth hormone

Eyes

Ophthalmologic eval Annually

ENT

Audiology eval Annually; more frequent eval if history of multiple episodes of otitis media

Renal

Blood pressure measurement Annually Assessment of renal function incl plasma BUN &

creatinine Annually Standard monitoring for renal anomalies Follow-up renal ultrasound if

symptomatic Sonographic eval for renal cysts In teenage/adult yrs as indicated by abnormalities on

renal function tests &/or blood pressure measurement Evaluation of Relatives at Risk See Genetic

Counseling for issues related to testing of at-risk relatives for genetic counseling

purposes. Pregnancy Management No specific pregnancy complications for the mother or the fetus

have been observed in the two women with SRCAP pathogenic variants who had children with

FHS. Therapies Under Investigation Search ClinicalTrials.gov in the US and EU Clinical Trials

Register in Europe for information on clinical studies for a wide range of diseases and conditions.

Note: There may not be clinical trials for this disorder.

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Referral of the family to support groups and other resources

Standard treatment for any of the following if identified:

Refractive errors and strabismus

Hearing loss

Seizures

Renal disease

Cryptorchidism

Orthopedic complications

Dental problems

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Investigation for celiac disease if indicated by clinical features

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Therapies Under Investigation Search ClinicalTrials.gov in the US and EU Clinical Trials Register in Europe for information on clinical studies for a wide range of diseases and conditions. Note: There may not be clinical trials for this disorder.

Genetic Counseling

Genetic counseling is the process of providing individuals and families with information on the nature, mode(s) of inheritance, and implications of genetic disorders to help them make informed medical and personal decisions. The following section deals with genetic risk assessment and the use of family history and genetic testing to clarify genetic status for family members; it is not meant to address all personal, cultural, or ethical issues that may arise or to substitute for consultation with a genetics professional. —ED.

Mode of Inheritance Floating-Harbor syndrome (FHS) is inherited in an autosomal dominant manner.

Risk to Family Members

Parents of a proband

Most individuals with FHS have the disorder as the result of a de novo SRCAP pathogenic variant and therefore represent simplex cases (i.e., a single occurrence in the family). Transmission of an SRCAP pathogenic variant from an affected mother to her child has been reported in two families to date [Nikkel et al 2013]. Molecular genetic testing and clinical evaluation for signs of FHS are recommended for the parents of a proband with an apparent de novo pathogenic variant. If the pathogenic variant found in the proband cannot be detected in the leukocyte DNA of either parent,

the proband most likely has a de novo pathogenic variant; another possible explanation is germline mosaicism in a parent. Though theoretically possible, no instances of germline mosaicism have been reported. The family history of some individuals diagnosed with FHS may appear to be negative because of failure to recognize the disorder in a family member with a milder phenotype. Therefore, an apparently negative family history cannot be confirmed unless appropriate clinical evaluation and/or molecular genetic testing has been performed on the parents of the proband. An advanced paternal age effect is suggested. In their series of 13 individuals with a heterozygous SRCAP pathogenic variant, Hood et al [2012] reported a mean paternal age of 36.9 years (range 29-44 years). Sibs of a proband. The risk to the sibs of the proband depends on the clinical/genetic status of the proband's parents: In the rare case of a parent being affected and/or known to have the pathogenic variant identified in the proband, the risk to sibs is 50%. If the proband has a known SRCAP pathogenic variant that cannot be detected in the leukocyte DNA of either parent, the recurrence risk to sibs is estimated to be 1% because of the theoretic possibility of parental germline mosaicism [Rahbari et al 2016]. Offspring of a proband. Each child of an individual with FHS has a 50% chance of inheriting the SRCAP pathogenic variant. Other family members. The risk to other family members depends on the status of the proband's parents: if a parent has the FHS-causing pathogenic variant, the parent's family members may be at risk. Related Genetic Counseling Issues Considerations in families with an apparent de novo pathogenic variant. When neither parent of a proband with an autosomal dominant condition has the pathogenic variant identified in the proband or clinical evidence of the disorder, the pathogenic variant is likely de novo. However, non-medical explanations including alternate paternity or maternity (e.g., with assisted reproduction) and undisclosed adoption could also be explored.

Family planning

The optimal time for determination of genetic risk and discussion of the availability of prenatal/preimplantation genetic testing is before pregnancy. It is appropriate to offer genetic counseling (including discussion of potential risks to offspring and reproductive options) to the parents of an affected child and to young adults who are affected. Prenatal Testing and

Preimplantation Genetic Testing Once the SRCAP pathogenic variant has been identified in an affected family member, prenatal testing for a pregnancy at increased risk for FHS and preimplantation genetic testing are possible. Differences in perspective may exist among medical professionals and within families regarding the use of prenatal testing. While most centers would consider use of prenatal testing to be a personal decision, discussion of these issues may be helpful.

Mode of Inheritance Floating-Harbor syndrome (FHS) is inherited in an autosomal dominant manner.

Risk to Family Members

Parents of a proband

Most individuals with FHS have the disorder as the result of a de novo SRCAP pathogenic variant and therefore represent simplex cases (i.e., a single occurrence in the family). Transmission of an SRCAP pathogenic variant from an affected mother to her child has been reported in two families to date [Nikkel et al 2013]. Molecular genetic testing and clinical evaluation for signs of FHS are recommended for the parents of a proband with an apparent de novo pathogenic variant. If the pathogenic variant found in the proband cannot be detected in the leukocyte DNA of either parent, the proband most likely has a de novo pathogenic variant; another possible explanation is germline mosaicism in a parent. Though theoretically possible, no instances of germline mosaicism have been reported. The family history of some individuals diagnosed with FHS may appear to be negative because of failure to recognize the disorder in a family member with a milder phenotype. Therefore, an apparently negative family history cannot be confirmed unless appropriate clinical evaluation and/or molecular genetic testing has been performed on the parents of the proband. An advanced paternal age effect is suggested. In their series of 13 individuals with a heterozygous SRCAP pathogenic variant, Hood et al [2012] reported a mean paternal age of 36.9 years (range 29-44 years).

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Molecular genetic testing and clinical evaluation for signs of FHS are recommended for the parents of a proband with an apparent de novo pathogenic variant.

If the pathogenic variant found in the proband cannot be detected in the leukocyte DNA of either parent, the proband most likely has a de novo pathogenic variant; another possible explanation is germline mosaicism in a parent. Though theoretically possible, no instances of germline mosaicism have been reported.

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Related Genetic Counseling Issues Considerations in families with an apparent de novo pathogenic variant. When neither parent of a proband with an autosomal dominant condition has the pathogenic variant identified in the proband or clinical evidence of the disorder, the pathogenic variant is likely de novo. However, non-medical explanations including alternate paternity or maternity (e.g., with assisted reproduction) and undisclosed adoption could also be explored.

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Resources

GeneReviews staff has selected the following disease-specific and/or umbrella support organizations and/or registries for the benefit of individuals with this disorder and their families. GeneReviews is not responsible for the information provided by other organizations. For information on selection criteria, [click here](#).

Human Growth Foundation

www.hgfound.org

MAGIC Foundation

Phone: 800-362-4423 Email: contactus@magicfoundation.org

www.magicfoundation.org

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Molecular Genetics Information in the Molecular Genetics and OMIM tables may differ from that elsewhere in the GeneReview: tables may contain more recent information. —ED. Table A. Floating-Harbor Syndrome: Genes and Databases View in own window Gene Chromosome Locus Protein Locus-Specific Databases HGMD ClinVar

SRCAP

16p11​.2

Helicase SRCAP

SRCAP @ LOVD

SRCAP

SRCAP

Data are compiled from the following standard references: gene from

HGNC;

chromosome locus from

OMIM;

protein from UniProt.

For a description of databases (Locus Specific, HGMD, ClinVar) to which links are provided, click [here](#).
Table B.OMIM Entries for Floating-Harbor Syndrome (View All in OMIM) View in own window

136140FLOATING-HARBOR SYNDROME; FLHS

611421SNF2-RELATED CBP ACTIVATOR PROTEIN; SRCAPMolecular PathogenesisIntroduction.

Helicase SRCAP is a nuclear protein that mediates different intracellular signaling pathways as well as chromatin remodeling. The encoded protein is an ATPase that is necessary for the incorporation of a histone variant into nucleosomes.SRCAP functions as a transcriptional activator for CREB and CBP-mediated transcription, along with Notch-mediated and steroid receptor-mediated transcription [Hood et al 2016]. Alteration in SRCAP has the potential for producing widespread target-gene

dysregulation.Mechanism of disease causation. Unknown. However, the non-random clustering of pathogenic variants (see Genotype-Phenotype Correlations) that predict truncated SRCAP strongly suggests a dominant-negative disease mechanism due to loss of one or more critical domain(s) – for instance, the three C-terminal AT-hook DNA-binding motifs (see Hood et al [2016] for details of SRCAP domains).Table 5. Notable SRCAP Pathogenic VariantsView in own

windowReference SequencesDNA Nucleotide ChangePredicted Protein ChangeComment
[Reference]

NM_006662​.2

NP_006653​.2

c.7303C>Tp.Arg2435TerRecurrent pathogenic variants [Hood et al 2012, Nikkel et al

2013]c.7330C>Tp.Arg2444TerVariants listed in the table have been provided by the authors.

GeneReviews staff have not independently verified the classification of variants.GeneReviews follows the standard naming conventions of the Human Genome Variation Society

(varnomen​.hgvs.org). See Quick Reference for an explanation of nomenclature.Cancer and Benign TumorsThe Cancer Genome Atlas summarizes somatic pathogenic variants in genes

(including SRCAP) involved in chromatin remodeling which may have a role in regulating genes in human malignancies. SRCAP is frequently mutated in numerous cancers including melanomas, lung cancers, stomach adenocarcinoma, and colorectal adenocarcinoma [Chen et al 2016].

Table A.Floating-Harbor Syndrome: Genes and DatabasesView in own windowGeneChromosome
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Floating-Harbor Syndrome: Genes and Databases

GeneChromosome LocusProteinLocus-Specific DatabasesHGMDClinVar

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Table B.OMIM Entries for Floating-Harbor Syndrome (View All in OMIM) [View in own window](#)

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Table 5. Notable SRCAP Pathogenic Variants

View in own window	Reference	Sequences	DNA Nucleotide Change	Predicted Protein Change	Comment [Reference]
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Notable SRCAP Pathogenic Variants

Reference	Sequences	DNA Nucleotide Change	Predicted Protein Change	Comment
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[Reference]				
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NM_006662				
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NP_006653				
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